<400> 1
gaattcgaaa cg atg cgt ctg ctg tct acc ttc act gaa tac atc aag aac 51
            Met Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn
             1   5   10

atc atc aat acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg   99

```
     Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu
         15                  20                  25

     atc gac ctg tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt     147
     Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val
      30                  35                  40                  45

     aac ttc gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa     195
     Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu
                     50                  55                  60

     tct tcc aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct     243
     Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser
                 65                  70                  75

     atg tac gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac     291
     Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr
             80                  85                  90

     ttc aac tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg     339
     Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met
         95                  100                 105

     gaa aac aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc     387
     Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile
     110                 115                 120                 125

     tgg act ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa     435
     Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys
                     130                 135                 140

     tac tct cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc     483
     Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe
                 145                 150                 155

     gtt acc atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac     531
     Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn
                 160                 165                 170

     ggc cgt ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac     579
     Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His
         175                 180                 185

     gct tct aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac     627
     Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His
     190                 195                 200                 205

     cgc tac atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac     675
     Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn
                     210                 215                 220

     gaa aaa gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc     723
     Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile
                 225                 230                 235

     ctg aaa gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac     771
     Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr
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                240                     245                     250

atg ctg aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta    819
Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val
    255                 260                 265

ggt atc cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg    867
Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met
270                 275                 280                 285

act acc aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc    915
Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe
                290                 295                 300

atc atc aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac    963
Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn
            305                 310                 315

aat gat cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt   1011
Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg
            320                 325                 330

ctg gct acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct   1059
Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala
    335                 340                 345

ctg gaa atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa   1107
Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys
350                 355                 360                 365

tcc aag aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag   1155
Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln
                370                 375                 380

gac aac aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac   1203
Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn
            385                 390                 395

aat atc gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa   1251
Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu
            400                 405                 410

cgt tcc tct cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat   1299
Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp
    415                 420                 425

gac ggt tgg ggt gaa cgt ccg ctg taa gaattc                        1332
Asp Gly Trp Gly Glu Arg Pro Leu  *
430                 435
```

<210> 2
<211> 437
<212> PRT
<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
      on BoNTA Hc

<400> 2
Met Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn
 1   5   10   15
Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
             20   25   30
Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
         35   40   45
Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
     50   55   60
Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
65   70   75   80
Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
                 85   90   95
Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
             100   105   110
Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
         115   120   125
Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
     130   135   140
Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
145   150   155   160
Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
             165   170   175
Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
         180   185   190
Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
         195   200   205
Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
     210   215   220
Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
225   230   235   240
Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn
             245   250   255
Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg
         260   265   270
Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn
     275   280   285
Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys
     290   295   300
Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg
305   310   315   320
Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr
             325   330   335
Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile
         340   345   350
Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn
     355   360   365
Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn
     370   375   380
Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala
385   390   395   400
Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser
             405   410   415
Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp

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              420             425             430
Gly Glu Arg Pro Leu
        435


<210> 3
<211> 1323
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (13)...(1314)

<400> 3
gaattcgaaa cg atg tct acc ttc act gaa tac atc aag aac atc atc aat  51
           Met Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn
            1               5                  10

acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg atc gac ctg    99
Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
     15              20                  25

tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt aac ttc gat   147
Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
 30              35                  40                  45

ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa tct tcc aaa   195
Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
                50                  55                  60

atc gaa gtt atc ctg aag aat gct atc gta tac aac tct atg tac gaa   243
Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
                65                  70                  75

aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac tcc   291
Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
            80                  85                  90

atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac aat   339
Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
     95                  100                 105

tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act ctg   387
Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
110                 115                 120                 125

cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa tac tct cag   435
Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
                130                 135                 140

atg atc aac atc tct gac tac atc aat cgc tgg atc ttc gtt acc atc   483
Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
                145                 150                 155
```

```
acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac ggc cgt ctg      531
Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
        160                 165                 170

atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac gct tct aat      579
Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
    175                 180                 185

aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac atc      627
Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
190                 195                 200                 205

tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac gaa aaa gaa      675
Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
                210                 215                 220

atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc ctg aaa gac      723
Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
                225                 230                 235

ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac atg ctg aat      771
Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn
        240                 245                 250

ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta ggt atc cgc      819
Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg
        255                 260                 265

ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg act acc aac      867
Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn
270                 275                 280                 285

atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc atc atc aag      915
Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys
                290                 295                 300

aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac aat gat cgt      963
Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg
                305                 310                 315

gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt ctg gct acc     1011
Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr
                320                 325                 330

aat gct tct cag gct ggt gta gaa aag atc ttg tct gct ctg gaa atc     1059
Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile
                335                 340                 345

ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa tcc aag aac     1107
Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn
350                 355                 360                 365

gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag gac aac aat     1155
Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn
                370                 375                 380

ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac aat atc gct     1203
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```
Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala
            385                 390                 395

aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa cgt tcc tct    1251
Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser
        400                 405                 410

cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat gac ggt tgg    1299
Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp
    415                 420                 425

ggt gaa cgt ccg ctg taagaattc                                       1323
Gly Glu Arg Pro Leu
430
```

<210> 4
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
      on BoNTA Hc

<400> 4
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Met Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile
 1               5                  10                  15
Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr
        20                  25                  30
Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp
        35                  40                  45
Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val
    50                  55                  60
Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser
65                  70                  75                  80
Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu
                85                  90                  95
Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp
            100                 105                 110
Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr
        115                 120                 125
Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn
    130                 135                 140
Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn
145                 150                 155                 160
Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln
            165                 170                 175
Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met
        180                 185                 190
Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys
        195                 200                 205
Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp
    210                 215                 220
Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly
225                 230                 235                 240
Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp
```

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                    245                    250                           255
Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met
                260                        265                   270
Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu
            275                    280                   285
Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala
        290                    295                300
Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile
305                    310                    315                    320
Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser
                325                    330                    335
Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val
            340                    345                   350
Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly
            355                    360                   365
Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp
        370                    375                380
Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val
385                    390                    395                    400
Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu
                405                    410                   415
Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg
                420                    425                   430
Pro Leu


<210> 5
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (13)...(1317)

<400> 5
gaattcgaaa cg atg gcc tct acc ttc act gaa tac atc aag aac atc atc   51
              Met Ala Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile
               1               5                   10

aat acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg atc gac    99
Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp
        15                  20                  25

ctg tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt aac ttc   147
Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe
 30                  35                  40                  45

gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa tct tcc   195
Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser
                50                  55                  60

aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct atg tac   243
Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr
```

```
                    65                    70                    75

gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac    291
Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn
             80                    85                    90

tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac    339
Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn
         95                   100                   105

aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act    387
Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr
110                   115                   120                   125

ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa tac tct    435
Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser
                 130                   135                   140

cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc gtt acc    483
Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr
             145                   150                   155

atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac ggc cgt    531
Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg
         160                   165                   170

ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac gct tct    579
Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser
         175                   180                   185

aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac    627
Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr
190                   195                   200                   205

atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac gaa aaa    675
Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys
                 210                   215                   220

gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc ctg aaa    723
Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys
             225                   230                   235

gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac atg ctg    771
Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu
             240                   245                   250

aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta ggt atc    819
Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile
         255                   260                   265

cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg act acc    867
Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr
270                   275                   280                   285

aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc atc atc    915
Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile
                 290                   295                   300
```

```
aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac aat gat        963
Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp
            305             310             315

cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt ctg gct       1011
Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala
            320             325             330

acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct ctg gaa       1059
Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu
            335             340             345

atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa tcc aag       1107
Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys
350             355             360             365

aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag gac aac       1155
Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn
                370             375             380

aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac aat atc       1203
Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile
            385             390             395

gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa cgt tcc       1251
Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser
        400             405             410

tct cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat gac ggt       1299
Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly
    415             420             425

tgg ggt gaa cgt ccg ctg taagaattc                                     1326
Trp Gly Glu Arg Pro Leu
430             435


<210> 6
<211> 435
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
      on BoNTA Hc

<400> 6
Met Ala Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser
 1               5                  10                  15
Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg
            20                  25                  30
Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile
            35                  40                  45
Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu
    50                  55                  60
Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe
```

```
        65                      70                      75                      80
Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser
                85                      90                      95
Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly
                100                     105                     110
Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp
                115                     120                     125
Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile
                130                     135                     140
Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn
145                     150                     155                     160
Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp
                165                     170                     175
Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile
                180                     185                     190
Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile
                195                     200                     205
Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys
                210                     215                     220
Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp
225                     230                     235                     240
Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr
                245                     250                     255
Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr
                260                     265                     270
Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr
                275                     280                     285
Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr
                290                     295                     300
Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr
305                     310                     315                     320
Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala
                325                     330                     335
Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp
                340                     345                     350
Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln
                355                     360                   ' 365
Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn
                370                     375                     380
Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu
385                     390                     395                     400
Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr
                405                     410                     415
Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu
                420                     425                     430
Arg Pro Leu
            435
```

<210> 7
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<400> 7

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gaattcacg atg gcc aac aaa tac aat tcc gaa atc ctg aac aat atc atc 51
          Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile
          1               5                   10

ctg aac ctg cgt tac aaa gac aac aat ctg atc gat ctg tct ggt tac   99
Leu Asn Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr
 15               20                  25                  30

ggt gct aaa gtt gaa gta tac gac ggt gtt gaa ctg aat gac aag aac   147
Gly Ala Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn
                 35                  40                  45

cag ttc aaa ctg acc tct tcc gct aac tct aag atc cgt gtt act cag   195
Gln Phe Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln
             50                  55                  60

aat cag aac atc atc ttc aac tcc gta ttc ctg gac ttc tct gtt tcc   243
Asn Gln Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser
             65                  70                  75

ttc tgg atc cgt atc ccg aaa tac aag aac gac ggt atc cag aat tac   291
Phe Trp Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr
         80                  85                  90

atc cac aat gaa tac acc atc atc aac tgc atg aag aat aac tct ggt   339
Ile His Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly
 95                  100                 105                 110

tgg aag atc tcc atc cgc ggt aac cgt atc atc tgg act ctg atc gat   387
Trp Lys Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp
             115                 120                 125

atc aac ggt aag acc aaa tct gta ttc ttc gaa tac aac atc cgt gaa   435
Ile Asn Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu
             130                 135                 140

gac atc tct gaa tac atc aat cgc tgg ttc ttc gtt acc atc acc aat   483
Asp Ile Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn
             145                 150                 155

aac ctg aac aat gct aaa atc tac atc aac ggt aaa ctg gaa tct aat   531
Asn Leu Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn
         160                 165                 170

acc gac atc aaa gac atc cgt gaa gtt atc gct aac ggt gaa atc atc   579
Thr Asp Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile
175                 180                 185                 190

ttc aaa ctg gac ggt gac atc gat cgt acc cag ttc atc tgg atg aaa   627
Phe Lys Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys
                 195                 200                 205

tac ttc tcc atc ttc aac acc gaa ctg tct cag tcc aat atc gaa gaa   675
```

```
Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu
            210                 215                 220

cgg tac aag atc cag tct tac tcc gaa tac ctg aaa gac ttc tgg ggt    723
Arg Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly
            225                 230                 235

aat ccg ctg atg tac aac aaa gaa tac tat atg ttc aat gct ggt aac    771
Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn
            240                 245                 250

aag aac tct tac atc aaa ctg aag aaa gac tct ccg gtt ggt gaa atc    819
Lys Asn Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile
255                 260                 265                 270

ctg act cgt tcc aaa tac aac cag aac tct aaa tac atc aac tac cgc    867
Leu Thr Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg
                275                 280                 285

gac ctg tac atc ggt gaa aag ttc atc atc cgt cgc aaa tct aac tct    915
Asp Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser
            290                 295                 300

cag tcc atc aat gat gac atc gta cgt aaa gaa gac tac atc tac ctg    963
Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu
            305                 310                 315

gac ttc ttc aac ctg aat cag gaa tgg cgt gta tac acc tac aag tac    1011
Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr
            320                 325                 330

ttc aag aaa gaa gaa gaa aag ctt ttc ctg gct ccg atc tct gat tcc    1059
Phe Lys Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser
335                 340                 345                 350

gac gaa ctc tac aac acc atc cag atc aaa gaa tac gac gaa cag ccg    1107
Asp Glu Leu Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro
                355                 360                 365

acc tac tct tgc cag ctg ctg ttc aag aaa gat gaa gaa tct act gac    1155
Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp
                370                 375                 380

gaa atc ggt ctg atc ggt atc cac cgt ttc tac gaa tct ggt atc gta    1203
Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val
            385                 390                 395

ttc gaa gaa tac aaa gac tac ttc tgc atc tcc aaa tgg tac ctg aag    1251
Phe Glu Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys
            400                 405                 410

gaa gtt aaa cgc aaa ccg tac aac ctg aaa ctg ggt tgc aat tgg cag    1299
Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln
415                 420                 425                 430

ttc atc ccg aaa gac gaa ggt tgg acc gaa tagtaagaat tc               1341
Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu
```

<210> 8
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
      on BoNTB Hc

<400> 8
Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn
 1   5   10   15
Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala
            20   25   30
Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn Gln Phe
        35   40   45
Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln Asn Gln
    50   55   60
Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser Phe Trp
65   70   75   80
Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr Ile His
                85   90   95
Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly Trp Lys
            100   105   110
Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Ile Asn
        115   120   125
Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile
    130   135   140
Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn Asn Leu
145   150   155   160
Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp
                165   170   175
Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys
            180   185   190
Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe
        195   200   205
Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr
    210   215   220
Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro
225   230   235   240
Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn
                245   250   255
Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Thr
                260   265   270
Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu
        275   280   285
Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser
    290   295   300
Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe
305   310   315   320
Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr Phe Lys
                325   330   335
Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu
            340   345   350

```
Leu Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro Thr Tyr
        355                 360                 365
Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile
        370                 375                 380
Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu
385                 390                 395                 400
Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val
                405                 410                 415
Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile
                420                 425                 430
Pro Lys Asp Glu Gly Trp Thr Glu
        435                 440
```

<210> 9
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (10)...(1359)

<400> 9

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gaattcacg atg acc atc cca ttc aac atc ttc tcc tac acc aac aac tcc   51
          Met Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser
           1               5                  10

ctg ttg aag gac atc atc aac gag tac ttc aac aac atc aac gac tcc     99
Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn Asp Ser
 15                 20                  25                  30

aag atc ctg tcc ctg cag aac cgt aag aac acc ttg gtc gac acc tcc    147
Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp Thr Ser
                35                  40                  45

ggt tac aac gcc gag gtc tcc gag gag ggt gac gtc cag ctg aac cca    195
Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu Asn Pro
                50                  55                  60

atc ttc cca ttc gac ttc aag ctg ggt tcc tcc ggt gag gac aga ggt    243
Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp Arg Gly
                65                  70                  75

aag gtc atc gtc acc cag aac gag aac atc gtc tac aac tcc atg tac    291
Lys Val Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser Met Tyr
         80                  85                  90

gag tcc ttc tcc atc tcc ttc tgg atc aga atc aac aag tgg gtc tcc    339
Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp Val Ser
 95                 100                 105                 110

aac ttg cca ggt tac acc atc atc gac tcc gtc aag aac aac tcc ggt    387
Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn Ser Gly
                115                 120                 125
```

```
tgg tcc atc ggt atc atc tcc aac ttc ctg gtc ttc acc ctg aag cag      435
Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu Lys Gln
            130             135             140

aac gag gac tcc gag cag tcc atc aac ttc tcc tac gac atc tcc aac      483
Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile Ser Asn
            145             150             155

aac gct cct ggt tac aac aag tgg ttc ttc gtc acc gtc acc aac aac      531
Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr Asn Asn
         160             165             170

atg atg ggt aac atg aag atc tac atc aac ggt aag ctg atc gac acc      579
Met Met Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile Asp Thr
175             180             185             190

atc aag gtc aag gag ttg acc ggt atc aac ttc tcc aag acc atc acc      627
Ile Lys Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr Ile Thr
            195             200             205

ttc gag atc aac aag atc cca gac acc ggt ctg atc acc tcc gac tcc      675
Phe Glu Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser
            210             215             220

gac aac atc aac atg tgg atc cgt gac ttc tac atc ttc gcc aag gag      723
Asp Asn Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu
            225             230             235

ttg gac ggt aag gac atc aac atc ctg ttc aac tcc ttg cag tac acc      771
Leu Asp Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr
         240             245             250

aac gtc gtc aag gac tac tgg ggt aac gac ctg aga tac aac aag gag      819
Asn Val Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu
255             260             265             270

tac tac atg gtc aac atc gac tac ttg aac aga tac atg tac gcc aac      867
Tyr Tyr Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn
            275             280             285

tcc aga cag atc gtc ttc aac acc aga cgt aac aac aac gac ttc aac      915
Ser Arg Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn
            290             295             300

gag ggt tac aag atc atc atc aag cgt atc aga ggt aac acc aac gac      963
Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn Asp
            305             310             315

acc aga gtc aga ggt ggt gac atc ctg tac ttc gac atg act atc aac     1011
Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr Ile Asn
         320             325             330

aac aag gcc tac aac ctg ttc atg aag aac gag acc atg tac gcc gac     1059
Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr Ala Asp
335             340             345             350
```

```
aac cac tcc acc gag gac atc tac gcc atc ggt ctg cgt gag cag acc    1107
Asn His Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu Gln Thr
            355             360             365

aag gac atc aac gac aac atc atc ttc cag atc cag cca atg aac aac    1155
Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met Asn Asn
            370             375             380

act tac tac tac gct tcc cag atc ttc aag tcc aac ttc aac ggt gag    1203
Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu
            385             390             395

aac atc tcc ggt atc tgt tcc atc ggt acc tac aga ttc cgt ctg ggt    1251
Asn Ile Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly
    400             405             410

ggt gac tgg tac aga cac aac tac ttg gtt cca act gtc aag cag ggt    1299
Gly Asp Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys Gln Gly
415             420             425             430

aac tac gcc tcc ttg ctg gag tcc act tcc acc cac tgg gga ttc gtc    1347
Asn Tyr Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly Phe Val
            435             440             445

cca gtc tcc gag taataggaat tc                                      1371
Pro Val Ser Glu
            450
```

<210> 10
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
      on BoNTC Hc

```
<400> 10
Met Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu
 1               5                  10                  15
Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn Asp Ser Lys Ile
            20                  25                  30
Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp Thr Ser Gly Tyr
            35                  40                  45
Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu Asn Pro Ile Phe
            50                  55                  60
Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp Arg Gly Lys Val
65                  70                  75                  80
Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser Met Tyr Glu Ser
                85                  90                  95
Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp Val Ser Asn Leu
            100                 105                 110
Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn Ser Gly Trp Ser
            115                 120                 125
Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu Lys Gln Asn Glu
            130                 135                 140
```

```
Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile Ser Asn Asn Ala
145                 150                 155                 160
Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr Asn Asn Met Met
                165                 170                 175
Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile Asp Thr Ile Lys
                180                 185                 190
Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr Ile Thr Phe Glu
                195                 200                 205
Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser Asp Asn
    210                 215                 220
Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu Leu Asp
225                 230                 235                 240
Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr Asn Val
                245                 250                 255
Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu Tyr Tyr
                260                 265                 270
Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn Ser Arg
        275                 280                 285
Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn Glu Gly
        290                 295                 300
Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn Asp Thr Arg
305                 310                 315                 320
Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr Ile Asn Asn Lys
                325                 330                 335
Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr Ala Asp Asn His
                340                 345                 350
Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu Gln Thr Lys Asp
        355                 360                 365
Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met Asn Asn Thr Tyr
    370                 375                 380
Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu Asn Ile
385                 390                 395                 400
Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly Gly Asp
                405                 410                 415
Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys Gln Gly Asn Tyr
                420                 425                 430
Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly Phe Val Pro Val
        435                 440                 445
Ser Glu
450


<210> 11
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (10)...(1362)

<400> 11
gaattcacg atg cgt ttg aag gct aag gtc aac gag tcc ttc gag aac acc 51
          Met Arg Leu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr
          1               5                   10
```

```
atg cca ttc aac atc ttc tcc tac acc aac aac tcc ttg ttg aag gac    99
Met Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp
 15              20              25              30

atc atc aac gag tac ttc aac tcc atc aac gac tcc aag atc ttg tcc   147
Ile Ile Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser
                 35              40              45

ttg cag aac aag aag aac gcc ttg gtc gac acc tcc ggt tac aac gcc   195
Leu Gln Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala
             50              55              60

gag gtc aga gtc ggt gac aac gtc cag ttg aac acc atc tac acc aac   243
Glu Val Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn
             65              70              75

gac ttc aag ttg tcc tct tcc ggt gac aag atc atc gtc aac ttg aac   291
Asp Phe Lys Leu Ser Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn
         80              85              90

aac aac atc ttg tac tcc gcc atc tac gag aac tcc tct gtc tcc ttc   339
Asn Asn Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe
 95              100             105             110

tgg atc aag atc tcc aag gac ttg acc aac tcc cac aac gag tac acc   387
Trp Ile Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr
                 115             120             125

atc atc aac tcc atc gag cag aac tcc ggt tgg aag ttg tgt atc cgt   435
Ile Ile Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg
                 130             135             140

aac ggt aac atc gag tgg atc ttg cag gac gtc aac cgt aag tac aag   483
Asn Gly Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys
             145             150             155

tcc ttg atc ttc gac tac tcc gag tcc ttg tcc cac acc ggt tac acc   531
Ser Leu Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr
             160             165             170

aac aag tgg ttc ttc gtc acc atc acc aac aac atc atg ggt tac atg   579
Asn Lys Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met
175             180             185             190

aag ttg tac atc aac ggt gag ttg aag cag tcc cag aag atc gag gac   627
Lys Leu Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp
                 195             200             205

ctg gac gag gtc aag ctg gac aag acc atc gtc ttc ggt atc gac gag   675
Leu Asp Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu
             210             215             220

aac atc gac gag aac cag atg ttg tgg atc cgt gac ttc aac atc ttc   723
Asn Ile Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe
             225             230             235
```

```
tcc aag gag ctg tcc aac gag gac atc aac atc gtc tac gag ggt cag     771
Ser Lys Glu Leu Ser Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln
    240             245             250

atc ctg agg aac gtc atc aag gac tac tgg ggt aac cca ctg aag ttc     819
Ile Leu Arg Asn Val Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe
255             260             265             270

gac acc gag tac tac atc atc aac gac aac tac atc gac cgt tac atc     867
Asp Thr Glu Tyr Tyr Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile
            275             280             285

gcc cca gag tcc aac gtc ctg gtc ctg gtc cag tac cct gac cgt tcc     915
Ala Pro Glu Ser Asn Val Leu Val Leu Val Gln Tyr Pro Asp Arg Ser
            290             295             300      .

aag ctg tac acc ggt aac cct atc acc atc aag tcc gtc tcc gac aag     963
Lys Leu Tyr Thr Gly Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys
        305             310             315

aac cct tac tcc cgt atc ctg aac ggt gac aac atc atc ctg cac atg    1011
Asn Pro Tyr Ser Arg Ile Leu Asn Gly Asp Asn Ile Ile Leu His Met
        320             325             330

ctg tac aac tcc cgt aag tac atg atc atc cgt gac acc gac acc atc    1059
Leu Tyr Asn Ser Arg Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile
335             340             345             350

tac gcc acc cag ggt ggt gac tgt tcc cag aac tgt gtc tac gcc ctg    1107
Tyr Ala Thr Gln Gly Gly Asp Cys Ser Gln Asn Cys Val Tyr Ala Leu
            355             360             365

aag ctg cag tcc aac ctg ggt aac tac ggt atc ggt atc ttc tcc atc    1155
Lys Leu Gln Ser Asn Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile
            370             375             380

aag aac atc gtc tcc aag aac aag tac tgc tcc cag atc ttc tcc tcc    1203
Lys Asn Ile Val Ser Lys Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser
        385             390             395

ttc cgt gag aac acc atg ctg ctg gcc gac atc tac aag cct tgg cgt    1251
Phe Arg Glu Asn Thr Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg
        400             405             410

ttc tcc ttc aag aac gcc tac act cct gtc gcc gtc acc aac tac gag    1299
Phe Ser Phe Lys Asn Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu
415             420             425             430

acc aag ctg ctg tcc acc tcc tcc ttc tgg aag ttc atc tcc cgt gac    1347
Thr Lys Leu Leu Ser Thr Ser Ser Phe Trp Lys Phe Ile Ser Arg Asp
            435             440             445

cca ggt tgg gtc gag taataggaat tc                                  1374
Pro Gly Trp Val Glu
        450
```

<210> 12
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
      on BoNTD Hc

<400> 12
Met Arg Leu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr Met Pro
1   5   10   15
Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile
            20   25   30
Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln
        35   40   45
Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val
    50   55   60
Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn Asp Phe
65   70   75   80
Lys Leu Ser Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn Asn Asn
                85   90   95
Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe Trp Ile
            100   105   110
Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr Ile Ile
        115   120   125
Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg Asn Gly
    130   135   140
Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys Ser Leu
145   150   155   160
Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr Asn Lys
                165   170   175
Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met Lys Leu
            180   185   190
Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp Leu Asp
        195   200   205
Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu Asn Ile
    210   215   220
Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe Ser Lys
225   230   235   240
Glu Leu Ser Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln Ile Leu
                245   250   255
Arg Asn Val Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe Asp Thr
            260   265   270
Glu Tyr Tyr Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile Ala Pro
        275   280   285
Glu Ser Asn Val Leu Val Leu Val Gln Tyr Pro Asp Arg Ser Lys Leu
    290   295   300
Tyr Thr Gly Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys Asn Pro
305   310   315   320
Tyr Ser Arg Ile Leu Asn Gly Asp Asn Ile Ile Leu His Met Leu Tyr
            325   330   335
Asn Ser Arg Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile Tyr Ala
            340   345   350
Thr Gln Gly Gly Asp Cys Ser Gln Asn Cys Val Tyr Ala Leu Lys Leu
        355   360   365
Gln Ser Asn Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile Lys Asn

```
            370                          375                         380
        Ile Val Ser Lys Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser Phe Arg
        385                          390                         395                         400
        Glu Asn Thr Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg Phe Ser
                             405                         410                         415
        Phe Lys Asn Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu Thr Lys
                         420                         425                         430
        Leu Leu Ser Thr Ser Ser Phe Trp Lys Phe Ile Ser Arg Asp Pro Gly
                     435                         440                         445
        Trp Val Glu
            450
```

<210> 13
<211> 1400
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (10)...(1356)

<400> 13

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gaattcacc atg gga gag agt cag caa gaa cta aat tct atg gta act gat   51
          Met Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr Asp
              1               5                       10

acc cta aat aat agt att cct ttt aag ctt tct tct tat aca gat gat   99
Thr Leu Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp Asp
 15                  20                  25                  30

aaa att tta att tcc tac ttc aac aag ttc ttc aag aga att aag tct   147
Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser
                 35                  40                  45

tct tcc gtt tta aac atg aga tac aag aat gat aaa tac gtc gac act   195
Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr
                 50                  55                  60

tcc ggt tac gac tcc aat atc aac att aac ggt gac gtg tac aag tac   243
Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr
             65                  70                  75

cca act aac aaa aac caa ttc ggt atc tac aac gac aag ctt act gag   291
Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Thr Glu
     80                  85                  90

ctg aac atc tct caa aac gac tac att atc tac gac aac aag tac aag   339
Leu Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys
 95                  100                 105                 110

aac ttc tct att tct ttc tgg gtc agg att cct aac tac gac aac aag   387
Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys
                 115                 120                 125
```

atc gtc aac gtt aac aac gag tac act atc atc aac tgt atg aga gac   435
Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp
            130   135   140

aac aac tcc ggt tgg aag gtc tct ctt aac cac aac gag atc att tgg   483
Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp
            145   150   155

acc ttg caa gac aac gca ggt att aac caa aag tta gca ttc aac tac   531
Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr
        160   165   170

ggt aac gca aac ggt att tct gac tac atc aac aag tgg att ttc gtc   579
Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val
175   180   185   190

act atc act aac gac aga tta ggt gac tct aag ctt tac att aac ggt   627
Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly
                195   200   205

aac tta atc gac caa aag tcc att tta aac tta ggt aac att cac gtt   675
Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val
            210   215   220

tct gac aac atc tta ttc aag atc gtt aac tgc agt tac acc aga tac   723
Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr
            225   230   235

att ggc att aga tac ttc aac att ttc gac aag gag tta gac gag acc   771
Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr
    240   245   250

gag att caa act tta tac agc aac gaa cct aac acc aat att ttg aag   819
Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys
255   260   265   270

gac ttc tgg ggt aac tac ttg ctt tac gac aag gaa tac tac tta tta   867
Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu
            275   280   285

aac gtg tta aag cca aac aac ttc att gat agg aga aag gat tct act   915
Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr
            290   295   300

tta agc att aac aac atc aga agc act att ctt tta gct aac aga tta   963
Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu
            305   310   315

tac tct ggt atc aag gtt aag atc caa aga gtt aac aac tct tct act   1011
Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr
        320   325   330

aac gat aac ctt gtt aga aag aac gat cag gtc tat att aac ttc gtc   1059
Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val
335   340   345   350

gct agc aag act cac tta ttc cca tta tat gct gat acc gct acc acc   1107

```
Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr
            355                 360                 365

aac aag gag aag acc atc aag atc tcc tcc tct ggc aac aga ttt aac    1155
Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn
            370                 375                 380

caa gtc gtc gtt atg aac tcc gtc ggt aac aac tgt acc atg aac ttt    1203
Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe
            385                 390                 395

aaa aat aat aat gga aat aat att ggg ttg tta ggt ttc aag gca gat    1251
Lys Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp
        400                 405                 410

act gta gtt gct agt act tgg tat tat acc cac atg aga gat cac acc    1299
Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr
415                 420                 425                 430

aac agc aat gga tgt ttt tgg aac ttt att tct gaa gaa cat gga tgg    1347
Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp
            435                 440                 445

caa gaa aaa taatagggat ccgcggccgc acgcgtcccg ggactagtga            1396
Gln Glu Lys

attc                                                               1400

<210> 14
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
      on BoNTE Hc

<400> 14
Met Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr Asp Thr Leu
 1               5                  10                  15
Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp Asp Lys Ile
            20                  25                  30
Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser Ser Ser
            35                  40                  45
Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr Ser Gly
        50                  55                  60
Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr Pro Thr
65                  70                  75                  80
Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Thr Glu Leu Asn
                85                  90                  95
Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys Asn Phe
            100                 105                 110
Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys Ile Val
            115                 120                 125
Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp Asn Asn
        130                 135                 140
```

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Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp Thr Leu
145                 150                 155                 160
Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr Gly Asn
                165                 170                 175
Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val Thr Ile
                180                 185                 190
Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly Asn Leu
                195                 200                 205
Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val Ser Asp
210                 215                 220
Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr Ile Gly
225                 230                 235                 240
Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr Glu Ile
                245                 250                 255
Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys Asp Phe
                260                 265                 270
Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu Asn Val
                275                 280                 285
Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr Leu Ser
                290                 295                 300
Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu Tyr Ser
305                 310                 315                 320
Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr Asn Asp
                325                 330                 335
Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val Ala Ser
                340                 345                 350
Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr Asn Lys
                355                 360                 365
Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn Gln Val
                370                 375                 380
Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe Lys Asn
385                 390                 395                 400
Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp Thr Val
                405                 410                 415
Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr Asn Ser
                420                 425                 430
Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp Gln Glu
                435                 440                 445
Lys
```

```
<210> 15
<211> 1317
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (10)...(1305)

<400> 15
gaattcacg atg tcc tac acc aac gac aag atc ctg atc ttg tac ttc aac 51
          Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn
           1               5                  10
```

```
aag ctg tac aag aag atc aag gac aac tcc atc ttg gac atg aga tac    99
Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr
 15              20              25              30

gaa aac aat aag ttc atc gac atc tcc ggt tac ggt tcc aac atc tcc   147
Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser
                35              40              45

atc aac ggt gac gtc tac atc tac tcc acc aat aga aac cag ttc gga   195
Ile Asn Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly
            50              55              60

atc tac tcc tcc aag cct tcc gag gtc aac atc gct cag aac aac gac   243
Ile Tyr Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp
        65              70              75

atc atc tac aac gga aga tac cag aac ttc tcc atc tcc ttc tgg gtc   291
Ile Ile Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val
    80              85              90

cgt atc cca aag tac ttc aac aag gtc aac ctg aat aac gag tac acc   339
Arg Ile Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr
 95             100             105             110

atc atc gac tgc atc cgt aac aat aac tcc gga tgg aag atc tcc ctg   387
Ile Ile Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu
            115             120             125

aac tac aac aag atc atc tgg acc ctg cag gac acc gcc ggt aac aat   435
Asn Tyr Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn
            130             135             140

cag aag ttg gtc ttc aac tac acc cag atg atc tcc atc tcc gac tac   483
Gln Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr
        145             150             155

atc aac aag tgg atc ttc gtc acc atc acc aat aac cgt ttg gga aac   531
Ile Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn
    160             165             170

tcc aga atc tac atc aac ggt aac ttg atc gac gag aag tcc atc tcc   579
Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser
175             180             185             190

aac ttg ggt gac atc cac gtc tcc gac aac att ttg ttc aag atc gtc   627
Asn Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val
            195             200             205

ggt tgt aac gac acc cgt tac gtc ggg atc cgt tac ttc aaa gtc ttc   675
Gly Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe
            210             215             220

gac act gag ttg ggt aag acc gag atc gag acc ttg tac tcc gac gag   723
Asp Thr Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu
        225             230             235
```

cct gac cca tcc atc ctg aag gac ttc tgg ggt aac tac ctg ctg tac 771
Pro Asp Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr
    240   245   250

aac aaa cgt tac tac ttg ctg aac ttg ttg cgt acc gac aag tcc atc 819
Asn Lys Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile
255   260   265   270

acc cag aac tcc aac ttc ttg aac atc aac cag cag aga ggt gtc tac 867
Thr Gln Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr
            275   280   285

cag aag cca aac atc ttc tcc aac acc aga ttg tac acc gga gtc gag 915
Gln Lys Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu
            290   295   300

gtc att atc aga aag aac gga tct act gat att tcc aac acc gat aac 963
Val Ile Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn
            305   310   315

ttc gtc aga aag aac gat ctg gct tac atc aac gtt gtc gac aga gat 1011
Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp
            320   325   330

gtc gaa tac cgt ctg tac gcc gat atc tct atc gcc aaa cct gaa aag 1059
Val Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys
335   340   345   350

atc atc aag ctg atc cgt acc tct aac tct aac aac tct ctg gga caa 1107
Ile Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln
            355   360   365

atc atc gtc atg gac tcc atc ggt aat aac tgt acc atg aac ttc cag 1155
Ile Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln
            370   375   380

aac aac aac ggt gga aac atc ggt ttg ttg ggt ttc cac tcc aac aac 1203
Asn Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn
            385   390   395

ttg gtc gct tcc tcc tgg tac tac aac aac atc cgt aag aac acc tcc 1251
Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser
            400   405   410

tcc aac ggt tgc ttc tgg tcc ttc atc tcc aag gag cac ggt tgg cag 1299
Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln
415   420   425   430

gag aac taataggaat tc 1317
Glu Asn

<210> 16
<211> 432
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
      on BoNTF Hc

<400> 16
Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu
 1   5   10   15
Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn
            20   25   30
Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn
            35   40   45
Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr
        50   55   60
Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile
65   70   75   80
Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile
                85   90   95
Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile
            100   105   110
Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr
        115   120   125
Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys
        130   135   140
Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn
145   150   155   160
Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg
                165   170   175
Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu
            180   185   190
Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys
        195   200   205
Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr
    210   215   220
Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp
225   230   235   240
Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys
                245   250   255
Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln
            260   265   270
Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys
            275   280   285
Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile
    290   295   300
Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val
305   310   315   320
Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu
            325   330   335
Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile
        340   345   350
Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile
        355   360   365
Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn
    370   375   380
Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val
385   390   395   400
Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn

```
                    405                 410                 415
    Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn
                420                 425                 430
```

```
aac aag tgg ttc tcc atc acc atc acc aac gac cgt ctg ggt aac gcc      531
Asn Lys Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala
    160             165             170

aac atc tac atc aac ggt tcc ctg aag aag tcc gag aag atc ctg aac      579
Asn Ile Tyr Ile Asn Gly Ser Leu Lys Lys Ser Glu Lys Ile Leu Asn
175             180             185             190

ctg gac cgt atc aac tcc tcc aac gac atc gac ttc aag ctg atc aac      627
Leu Asp Arg Ile Asn Ser Ser Asn Asp Ile Asp Phe Lys Leu Ile Asn
                195             200             205

tgt acc gac acc acc aag ttc gtc tgg atc aag gac ttc aac atc ttc      675
Cys Thr Asp Thr Thr Lys Phe Val Trp Ile Lys Asp Phe Asn Ile Phe
            210             215             220

ggt cgt gag ctg aac gcc acc gag gtc tcc tcc ctg tac tgg atc cag      723
Gly Arg Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln
        225             230             235

tcc tcc acc aac acc ctg aag gac ttc tgg gga aac cca ctg cgt tac      771
Ser Ser Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr
    240             245             250

gac acc cag tac tac ctg ttc aac cag ggt atg cag aac atc tac atc      819
Asp Thr Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile
255             260             265             270

aag tac ttc tcc aag gcc tcc atg ggt gag acc gcc cct cgt acc aac      867
Lys Tyr Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn
                275             280             285

ttc aac aac gcc gcc atc aac tac cag aac ctg tac ctg ggt ctg cgt      915
Phe Asn Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg
        290             295             300

ttc atc atc aag aag gcc tcc aac tcc cgt aac atc aac aac gac aac      963
Phe Ile Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn
        305             310             315

atc gtc cgt gag ggt gac tac atc tac ctg aac atc gac aac atc tcc     1011
Ile Val Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser
    320             325             330

gac gag tcc tac cgt gtc tac gtc ctg gtc aac tcc aag gag atc cag     1059
Asp Glu Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln
335             340             345             350

acc cag ctg ttc ctg gcc cca atc aac gac gac cct acc ttc tac gac     1107
Thr Gln Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp
                355             360             365

gtc ctg cag atc aag aag tac tac gag aag acc acc tac aac tgt cag     1155
Val Leu Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln
                370             375             380

atc ctg tgc gag aag gac acc aag acc ttc gga ctg ttc ggt atc ggt     1203
```

```
Ile Leu Cys Glu Lys Asp Thr Lys Thr Phe Gly Leu Phe Gly Ile Gly
        385                 390             395

aag ttc gtc aag gac tac ggt tac gtc tgg gac acc tac gac aac tac     1251
Lys Phe Val Lys Asp Tyr Gly Tyr Val Trp Asp Thr Tyr Asp Asn Tyr
    400                 405             410

ttc tgt atc tcc cag tgg tac ctg cgt cgt atc tcc gag aac atc aac     1299
Phe Cys Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu Asn Ile Asn
415                 420             425                 430

aag ctg cgt ctg gga tgt aac tgg cag ttc atc cca gtc gac gag ggt     1347
Lys Leu Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu Gly
                435             440             445

tgg acc gag taataggaat tc                                           1368
Trp Thr Glu
```

<210> 18
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
      on BoNTG Hc

<400> 18
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Met Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile Ser Asn
1               5                   10                  15
Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly Arg Leu
            20                  25                  30
Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser Asp Val
            35                  40                  45
Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn Ser Glu
    50                  55                  60
Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr Asp Ser
65                  70                  75                  80
Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro Lys Tyr
                85                  90                  95
Asn Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn Glu Tyr Thr Ile Ile
            100                 105                 110
Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys Gly Asn
    115                 120                 125
Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys Ser Ile
    130                 135                 140
Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile Asn Lys
145                 150                 155                 160
Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala Asn Ile
                165                 170                 175
Tyr Ile Asn Gly Ser Leu Lys Lys Ser Glu Lys Ile Leu Asn Leu Asp
            180                 185                 190
Arg Ile Asn Ser Ser Asn Asp Ile Asp Phe Lys Leu Ile Asn Cys Thr
    195                 200                 205
Asp Thr Thr Lys Phe Val Trp Ile Lys Asp Phe Asn Ile Phe Gly Arg
```

```
          210                      215                      220
Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln Ser Ser
225                      230                      235                      240
Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr
                245                      250                      255
Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile Lys Tyr
                260                      265                      270
Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn Phe Asn
                275                      280                      285
Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg Phe Ile
                290                      295                      300
Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn Ile Val
305                      310                      315                      320
Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser Asp Glu
                325                      330                      335
Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln Thr Gln
                340                      345                      350
Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp Val Leu
                355                      360                      365
Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln Ile Leu
                370                      375                      380
Cys Glu Lys Asp Thr Lys Thr Phe Gly Leu Phe Gly Ile Gly Lys Phe
385                      390                      395                      400
Val Lys Asp Tyr Gly Tyr Val Trp Asp Thr Tyr Asp Asn Tyr Phe Cys
                405                      410                      415
Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu Asn Ile Asn Lys Leu
                420                      425                      430
Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu Gly Trp Thr
                435                      440                      445
Glu
```

```
<400> 19
atg gct ctg aac gac ctg tgc atc aaa gtt aac aac tgg gac ctg ttc    48
Met Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe
 1               5                  10                  15


ttc tcc ccg tct gaa gac aac ttc act aac gac ctg aac aaa ggc gaa    96
Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu
                20                  25                  30


gaa atc acc tcc gac act aac atc gaa gct gct gaa gaa aac atc tct   144
Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser
                35                  40                  45
```

```
ctg gac ctg atc cag cag tac tac ctg act ttc aac ttc gac aac gaa      192
Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu
    50                  55                  60

ccg gaa aac atc tcc atc gaa aac ctg tct tcc gac atc atc ggt cag      240
Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln
65                  70                  75                  80

ctg gaa ctg atg ccg aac atc gaa cgc ttc ccg aac ggc aag aaa tac      288
Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr
                85                  90                  95

gaa ctg gac aaa tac acc atg ttc cac tac ctg cgt gct cag gaa ttc      336
Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe
                100                 105                 110

gaa cac ggt aaa tct cgt atc gct ctg act aac tcc gtt aac gaa gct      384
Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala
            115                 120                 125

ctg ctg aac ccg tct cgc gtt tac acc ttc ttc tct tcc gac tac gtt      432
Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val
    130                 135                 140

aag aaa gtt aac aaa gct act gaa gct gct atg ttc ctg ggt tgg gtt      480
Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val
145                 150                 155                 160

gaa cag ctg gtt tac gac ttc acc gac gaa act tct gaa gtt tcc acc      528
Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr
                165                 170                 175

act gac aaa atc gct gac atc act atc atc atc ccg tac atc ggc ccg      576
Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro
                180                 185                 190

gct ctg aac atc ggt aac atg ctg tac aaa gac gac ttc gtt ggt gct      624
Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala
            195                 200                 205

ctg atc ttc tct ggc gct gtt atc ctg ctg gaa ttc atc ccg gaa atc      672
Leu Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile
    210                 215                 220

gct atc ccg gtt ctg ggt acc ttc gct ctg gtt tcc tac atc gct aac      720
Ala Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn
225                 230                 235                 240

aaa gtt ctg act gtt cag acc atc gac aac gct ctg tct aaa cgt aac      768
Lys Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn
                245                 250                 255

gaa aaa tgg gac gaa gtt tac aaa tac atc gtt act aac tgg ctg gct      816
Glu Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala
                260                 265                 270

aaa gtt aac act cag atc gac ctg atc cgt aag aag atg aaa gaa gct      864
```

```
            Lys Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala
                    275                 280                 285

ctg gaa aac cag gct gaa gct act aaa gct atc atc aac tac cag tac        912
Leu Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr
        290                 295                 300

aac cag tac acc gaa gaa gaa aag aac aac atc aac ttc aac atc gat        960
Asn Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp
305                 310                 315                 320

gac ctg tcc tct aaa ctg aac gaa tcc atc aac aaa gct atg atc aac       1008
Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn
                325                 330                 335

atc aac aaa ttc ctg aac cag tgc tct gtt tcc tac ctg atg aac tct       1056
Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser
                340                 345                 350

atg atc ccg tac ggc gtt aaa cgc ctg gaa gac ttc gac gct tcc ctg       1104
Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu
                355                 360                 365

aaa gac gct ctg ctg aaa tac atc cgt gac aac tac ggt act ctg atc       1152
Lys Asp Ala Leu Leu Lys Tyr Ile Arg Asp Asn Tyr Gly Thr Leu Ile
                370                 375                 380

ggc cag gtt gac cgt ctg aaa gac aag gtt aac aac acc ctg tct act       1200
Gly Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr
385                 390                 395                 400

gac atc ccg ttc cag ctg tcc aaa tac gtt gac aac cag taa             1242
Asp Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln
                405                 410
```

<210> 20
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
      on BoNTA Hn

<400> 20
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Met Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe
1               5                   10                  15
Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu
            20                  25                  30
Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser
            35                  40                  45
Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu
        50                  55                  60
Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln
65                  70                  75                  80
Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr
```

```
                    85                    90                    95
Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe
                   100                   105                   110
Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala
                   115                   120                   125
Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val
                   130                   135                   140
Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val
145                   150                   155                   160
Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr
                   165                   170                   175
Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro
                   180                   185                   190
Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala
                   195                   200                   205
Leu Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile
                   210                   215                   220
Ala Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn
225                   230                   235                   240
Lys Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn
                   245                   250                   255
Glu Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala
                   260                   265                   270
Lys Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala
                   275                   280                   285
Leu Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr
                   290                   295                   300
Asn Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp
305                   310                   315                   320
Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn
                   325                   330                   335
Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser
                   340                   345                   350
Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu
                   355                   360                   365
Lys Asp Ala Leu Leu Lys Tyr Ile Arg Asp Asn Tyr Gly Thr Leu Ile
                   370                   375                   380
Gly Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr
385                   390                   395                   400
Asp Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln
                   405                   410


<210> 21
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (1)...(1239)

<400> 21
atg gct cca gga atc tgt atc gac gtc gac aac gag gac ttg ttc ttc    48
Met Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe
```

```
         1              5                   10                      15

atc gct gac aag aac tcc ttc tcc gac gac ttg tcc aag aac gag aga      96
Ile Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg
             20              25                  30

atc gag tac aac acc cag tcc aac tac atc gag aac gac ttc cca atc     144
Ile Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile
             35              40                  45

aac gag ttg atc ttg gac acc gac ttg atc tcc aag atc gag ttg cca     192
Asn Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro
         50              55                  60

tcc gag aac acc gag tcc ttg act gac ttc aac gtc gac gtc cca gtc     240
Ser Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val
65              70                  75                  80

tac gag aag caa cca gct atc aag aag att ttc acc gac gag aac acc     288
Tyr Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr
                 85                  90                  95

atc ttc caa tac ctg tac tct cag acc ttc cct ttg gac atc aga gac     336
Ile Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp
             100                 105                 110

atc tcc ttg acc tct tcc ttc gac gac gcc ctg ctg ttc tcc aac aag     384
Ile Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys
         115                 120                 125

gtc tac tcc ttc ttc tcc atg gac tac atc aag act gct aac aag gtc     432
Val Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val
         130                 135                 140

gtc gag gcc ggt ttg ttc gct ggt tgg gtc aag cag atc gtc aac gat     480
Val Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp
145                 150                 155                 160

ttc gtc atc gag gct aac aag tcc aac acc atg gac aag att gcc gac     528
Phe Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp
                 165                 170                 175

atc tcc ttg att gtc cca tac atc ggt ttg gcc ttg aac gtc ggt aac     576
Ile Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn
             180                 185                 190

gag acc gcc aag ggt aac ttc gag aac gct ttc gag atc gct ggt gcc     624
Glu Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala
         195                 200                 205

tcc atc ttg ttg gag ttc atc cca gag ttg ttg atc cca gtc gtc ggt     672
Ser Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly
         210                 215                 220

gcc ttc ttg ttg gag tcc tac atc gac aac aag aac aag atc atc aag     720
Ala Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys
225                 230                 235                 240
```

```
acc atc gac aac gct ttg acc aag aga aac gag aag tgg tcc gac atg    768
Thr Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met
                245                 250                 255

tac ggt ttg atc gtc gcc caa tgg ttg tcc acc gtc aac acc caa ttc    816
Tyr Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe
                260                 265                 270

tac acc atc aag gag ggt atg tac aag gcc ttg aac tac cag gcc caa    864
Tyr Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln
                275                 280                 285

gct ttg gag gag atc atc aag tac aga tac aac atc tac tcc gag aag    912
Ala Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys
            290                 295                 300

gag aag tcc aac att aac atc gac ttc aac gac atc aac tcc aag ctg    960
Glu Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu
305                 310                 315                 320

aac gag ggt att aac cag gcc atc gac aac atc aac aac ttc atc aac   1008
Asn Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn
                325                 330                 335

ggt tgt tcc gtc tcc tac ttg atg aag aag atg att cca ttg gcc gtc   1056
Gly Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val
                340                 345                 350

gag aag ttg ttg gac ttc gac aac acc ctg aag aag aac ttg ttg aac   1104
Glu Lys Leu Leu Asp Phe Asp Asn Thr Leu Lys Lys Asn Leu Leu Asn
                355                 360                 365

tac atc gac gag aac aag ttg tac ttg atc ggt tcc gct gag tac gag   1152
Tyr Ile Asp Glu Asn Lys Leu Tyr Leu Ile Gly Ser Ala Glu Tyr Glu
            370                 375                 380

aag tcc aag gtc aac aag tac ttg aag acc atc atg cca ttc gac ttg   1200
Lys Ser Lys Val Asn Lys Tyr Leu Lys Thr Ile Met Pro Phe Asp Leu
385                 390                 395                 400

tcc atc tac acc aac gac acc atc ttg atc gag atg ttc taa           1242
Ser Ile Tyr Thr Asn Asp Thr Ile Leu Ile Glu Met Phe
                405                 410
```

<210> 22
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
      on BoNTB Hn

<400> 22
Met Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe

Ile Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg
           20   25   30

Ile Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile
           35   40   45

Asn Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro
     50   55   60

Ser Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val
65   70   75   80

Tyr Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr
           85   90   95

Ile Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp
          100   105   110

Ile Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys
          115   120   125

Val Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val
          130   135   140

Val Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp
145   150   155   160

Phe Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp
          165   170   175

Ile Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn
          180   185   190

Glu Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala
          195   200   205

Ser Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly
          210   215   220

Ala Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys
225   230   235   240

Thr Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met
          245   250   255

Tyr Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe
          260   265   270

Tyr Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln
          275   280   285

Ala Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys
          290   295   300

Glu Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu
305   310   315   320

Asn Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn
          325   330   335

Gly Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val
          340   345   350

Glu Lys Leu Leu Asp Phe Asp Asn Thr Leu Lys Lys Asn Leu Leu Asn
          355   360   365

Tyr Ile Asp Glu Asn Lys Leu Tyr Leu Ile Gly Ser Ala Glu Tyr Glu
          370   375   380

Lys Ser Lys Val Asn Lys Tyr Leu Lys Thr Ile Met Pro Phe Asp Leu
385   390   395   400

Ser Ile Tyr Thr Asn Asp Thr Ile Leu Ile Glu Met Phe
          405   410

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (1)...(1197)

<400> 23

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atg tcc ctg tac aac aag acc ctt gac tgt aga gag ctg ctg gtg aag      48
Met Ser Leu Tyr Asn Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys
 1               5                   10                  15

aac act gac ctg cca ttc atc ggt gac atc agt gac gtg aag act gac      96
Asn Thr Asp Leu Pro Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp
             20                  25                  30

atc ttc ctg cgt aag gac atc aac gag gag act gag gtg atc tac tac     144
Ile Phe Leu Arg Lys Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr
         35                  40                  45

cca gac aac gtg tca gta gac caa gtg atc ctc agt aag aac acc tcc     192
Pro Asp Asn Val Ser Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser
     50                  55                  60

gag cat gga caa cta gac ctg ctc tac cct agt atc gac agt gag agt     240
Glu His Gly Gln Leu Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser
 65                  70                  75                  80

gag atc ctg cca ggg gag aat caa gtc ttc tac gac aac cgt acc cag     288
Glu Ile Leu Pro Gly Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln
                 85                  90                  95

aac gtg gac tac ctg aac tcc tac tac tac cta gag tct cag aag ctg     336
Asn Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu
            100                 105                 110

agt gac aac gtg gag gac ttc act ttc acg cgt tca atc gag gag gct     384
Ser Asp Asn Val Glu Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala
            115                 120                 125

ctg gac aac agt gca aag gtg tac act tac ttc cct acc ctg gct aac     432
Leu Asp Asn Ser Ala Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn
        130                 135                 140

aag gtg aat gcc ggt gtg caa ggt ggt ctg ttc ctg atg tgg gca aac     480
Lys Val Asn Ala Gly Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn
145                 150                 155                 160

gac gtg gtt gag gac ttc act acc aac atc ctg cgt aag gac aca ctg     528
Asp Val Val Glu Asp Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu
                165                 170                 175

gac aag atc tca gat gtg tca gct atc atc ccc tac atc gga ccc gca     576
Asp Lys Ile Ser Asp Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala
            180                 185                 190

ctg aac atc tcc aac tct gtg cgt cgt gga aac ttc act gag gca ttc     624
```

```
Leu Asn Ile Ser Asn Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe
        195                 200                 205

gca gtc act ggt gtc acc atc ctg ctg gag gca ttc cct gag ttc aca    672
Ala Val Thr Gly Val Thr Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr
        210                 215                 220

atc cct gct ctg ggt gca ttc gtg atc tac agt aag gtc cag gag cga    720
Ile Pro Ala Leu Gly Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg
225                 230                 235                 240

aac gag atc atc aag acc atc gac aac tgt ctg gag cag agg atc aag    768
Asn Glu Ile Ile Lys Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys
                245                 250                 255

aga tgg aag gac tcc tac gag tgg atg atg gga acg tgg ttg tcc agg    816
Arg Trp Lys Asp Ser Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg
                260                 265                 270

atc atc acc cag ttc aac aac atc tcc tac cag atg tac gac tcc ctg    864
Ile Ile Thr Gln Phe Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu
        275                 280                 285

aac tac cag gca ggt gca atc aag gct aag atc gac ctg gag tac aag    912
Asn Tyr Gln Ala Gly Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys
        290                 295                 300

aag tac tcc gga agc gac aag gag aac atc aag agc cag gtt gag aac    960
Lys Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn
305                 310                 315                 320

ctg aag aac agt ctg gac gtc aag atc tcg gag gca atg aac aac atc    1008
Leu Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile
                325                 330                 335

aac aag ttc atc cga gag tgc tcc gtc acc tac ctg ttc aag aac atg    1056
Asn Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met
        340                 345                 350

ctg cct aag gtc atc gac gag ctg aac gag ttc gac cga aac acc aag    1104
Leu Pro Lys Val Ile Asp Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys
        355                 360                 365

gca aag ctg atc aac ctg atc gac tcc cat aac atc atc ctg gtc ggt    1152
Ala Lys Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly
        370                 375                 380

gag gtc gac aag ctg aag gca aag gta aac aac agc ttc cag aac        1197
Glu Val Asp Lys Leu Lys Ala Lys Val Asn Asn Ser Phe Gln Asn
385                 390                 395

taa                                                                1200

<210> 24
<211> 399
<212> PRT
<213> Artificial Sequence
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<220>
<223> Encoded polypeptide of a synthetic construct based
      on BoNTC Hn

<400> 24
Met Ser Leu Tyr Asn Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys
 1   5   10   15
Asn Thr Asp Leu Pro Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp
            20   25   30
Ile Phe Leu Arg Lys Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr
        35   40   45
Pro Asp Asn Val Ser Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser
    50   55   60
Glu His Gly Gln Leu Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser
65   70   75   80
Glu Ile Leu Pro Gly Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln
            85   90   95
Asn Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu
            100   105   110
Ser Asp Asn Val Glu Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala
            115   120   125
Leu Asp Asn Ser Ala Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn
    130   135   140
Lys Val Asn Ala Gly Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn
145   150   155   160
Asp Val Val Glu Asp Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu
            165   170   175
Asp Lys Ile Ser Asp Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala
            180   185   190
Leu Asn Ile Ser Asn Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe
            195   200   205
Ala Val Thr Gly Val Thr Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr
    210   215   220
Ile Pro Ala Leu Gly Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg
225   230   235   240
Asn Glu Ile Ile Lys Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys
            245   250   255
Arg Trp Lys Asp Ser Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg
            260   265   270
Ile Ile Thr Gln Phe Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu
            275   280   285
Asn Tyr Gln Ala Gly Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys
    290   295   300
Lys Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn
305   310   315   320
Leu Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile
            325   330   335
Asn Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met
            340   345   350
Leu Pro Lys Val Ile Asp Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys
            355   360   365
Ala Lys Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly
    370   375   380
Glu Val Asp Lys Leu Lys Ala Lys Val Asn Asn Ser Phe Gln Asn
385   390   395

<210> 25
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (1)...(1158)

<400> 25
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atg gcc aac tcc cgt gac gac tcc acc tgc atc aag gtc aag aac aac      48
Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn
 1               5                  10                  15

aga ctg cca tac gtt gcc gac aag gac tcc atc tcc cag gag atc ttc      96
Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe
                20                  25                  30

gag aac aag atc atc acc gac gag acc aac gtt caa aac tac tcc gac     144
Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp
            35                  40                  45

aag ttc tct ttg gac gag tcc atc ctg gac ggt cag gtc cca atc aac     192
Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn
        50                  55                  60

cca gag atc gtc gac cca ctg ttg cca aac gtc aac atg gag cca ttg     240
Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu
65                  70                  75                  80

aac ttg cca ggt gag gag atc gtc ttc tac gac gac atc acc aag tac     288
Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr
                85                  90                  95

gtc gac tac ttg aac tcc tac tac tac ttg gag tct caa aag ttg tct     336
Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser
               100                 105                 110

aac aac gtc gag aac atc acc ttg acc acc tcc gtc gag gag gcc ttg     384
Asn Asn Val Glu Asn Ile Thr Leu Thr Thr Ser Val Glu Glu Ala Leu
           115                 120                 125

ggt tac tct aac aag atc tac acc ttc ctg cca tcc ttg gct gag aag     432
Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys
       130                 135                 140

gtt aac aag ggt gtt caa gct ggt ttg ttc ctg aac tgg gcc aac gag     480
Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu
145                 150                 155                 160

gtc gtc gag gac ttc acc acc aac atc atg aag aag gac acc ctg gac     528
Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp
                165                 170                 175
```

```
aag atc tcc gac gtc tcc gtc atc atc cca tac atc ggt cca gcc ttg      576
Lys Ile Ser Asp Val Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu
            180             185             190

aac atc ggt aac tcc gcc ctg aga ggt aac ttc aac cag gcc ttc gcc      624
Asn Ile Gly Asn Ser Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala
            195             200             205

acc gcc ggt gtc gcc ttc ctg ctg gag ggt ttc cca gag ttc acc atc      672
Thr Ala Gly Val Ala Phe Leu Leu Glu Gly Phe Pro Glu Phe Thr Ile
            210             215             220

cca gcc ctg ggt gtc ttc acc ttc tac tcc tcc atc cag gag aga gag      720
Pro Ala Leu Gly Val Phe Thr Phe Tyr Ser Ser Ile Gln Glu Arg Glu
225             230             235             240

aag atc atc aag acc atc gag aac tgc ttg gag cag aga gtc aag aga      768
Lys Ile Ile Lys Thr Ile Glu Asn Cys Leu Glu Gln Arg Val Lys Arg
            245             250             255

tgg aag gac tcc tac cag tgg atg gtt tcc aac tgg ctg tcc aga atc      816
Trp Lys Asp Ser Tyr Gln Trp Met Val Ser Asn Trp Leu Ser Arg Ile
            260             265             270

acc acc caa ttc aac cac atc aac tac cag atg tac gac tcc ctg tcc      864
Thr Thr Gln Phe Asn His Ile Asn Tyr Gln Met Tyr Asp Ser Leu Ser
            275             280             285

tac cag gcc gac gcc atc aag gcc aag atc gac ctg gag tac aag aag      912
Tyr Gln Ala Asp Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys
            290             295             300

tac tcc ggt tcc gac aag gag aac atc aag tcc cag gtc gag aac ctg      960
Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu
305             310             315             320

aag aac tcc ttg gac gtc aag atc tcc gag gcc atg aac aac atc aac     1008
Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn
            325             330             335

aag ttc atc cgt gag tgt tcc gtc acc tac ctg ttc aag aac atg ctg     1056
Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu
            340             345             350

cca aag gtc atc gac gag ctg aac aag ttc gac ctg aga acc aag acc     1104
Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr
            355             360             365

gag ctg atc aac ctg atc gac tcc cac aac atc atc ctg gtt ggt gag     1152
Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu
            370             375             380

gtt gac taa                                                          1161
Val Asp
385
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<210> 26
<211> 386
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
     on BoNTD Hn

<400> 26
Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn
 1   5   10   15
Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe
            20   25   30
Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp
        35   40   45
Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn
    50   55   60
Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu
65   70   75   80
Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr
                85   90   95
Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser
            100   105   110
Asn Asn Val Glu Asn Ile Thr Leu Thr Thr Ser Val Glu Glu Ala Leu
        115   120   125
Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys
    130   135   140
Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu
145   150   155   160
Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp
                165   170   175
Lys Ile Ser Asp Val Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu
            180   185   190
Asn Ile Gly Asn Ser Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala
        195   200   205
Thr Ala Gly Val Ala Phe Leu Leu Glu Gly Phe Pro Glu Phe Thr Ile
    210   215   220
Pro Ala Leu Gly Val Phe Thr Phe Tyr Ser Ser Ile Gln Glu Arg Glu
225   230   235   240
Lys Ile Ile Lys Thr Ile Glu Asn Cys Leu Glu Gln Arg Val Lys Arg
            245   250   255
Trp Lys Asp Ser Tyr Gln Trp Met Val Ser Asn Trp Leu Ser Arg Ile
            260   265   270
Thr Thr Gln Phe Asn His Ile Asn Tyr Gln Met Tyr Asp Ser Leu Ser
        275   280   285
Tyr Gln Ala Asp Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys
    290   295   300
Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu
305   310   315   320
Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn
                325   330   335
Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu
            340   345   350
Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr
            355   360   365
Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu

```
        370                375                380
Val Asp
385


<210> 27
<211> 1149
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (1)...(1146)

<400> 27
atg tcc atc tgc atc gag atc aac aac ggt gag ctg ttc ttc gtg gct    48
Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala
 1               5                  10                  15

tcc gag aac agt tac aac gat gac aac atc aac act cct aag gag att    96
Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile
                20                  25                  30

gac gac acc gtc act tct aac aac aac tac gaa aac gac ctg gac cag   144
Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr Glu Asn Asp Leu Asp Gln
            35                  40                  45

gtc atc cta aac ttc aac tcc gag tcc gcc cct ggt ctg tcc gac gag   192
Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu
        50                  55                  60

aag ctg aac ctg acc atc cag aac gac gct tac atc cca aag tac gac   240
Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala Tyr Ile Pro Lys Tyr Asp
 65                  70                  75                  80

tcc aac ggt aca tcc gat atc gag cag cat gac gtt aac gag ctt aac   288
Ser Asn Gly Thr Ser Asp Ile Glu Gln His Asp Val Asn Glu Leu Asn
                85                  90                  95

gtc ttc ttc tac tta gac gct cag aag gtg ccc gag ggt gag aac aac   336
Val Phe Phe Tyr Leu Asp Ala Gln Lys Val Pro Glu Gly Glu Asn Asn
                100                 105                 110

gtc aat ctc acc tct tca att gac aca gcc ttg ttg gag cag cct aag   384
Val Asn Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu Gln Pro Lys
            115                 120                 125

atc tac acc ttc ttc tcc tcc gag ttc atc aac aac gtc aac aag cct   432
Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile Asn Asn Val Asn Lys Pro
        130                 135                 140

gtg cag gcc gca ttg ttc gta agc tgg att cag cag gtg tta gta gac   480
Val Gln Ala Ala Leu Phe Val Ser Trp Ile Gln Gln Val Leu Val Asp
145                 150                 155                 160
```

```
ttc act act gag gct aac cag aag tcc act gtt gac aag atc gct gac      528
Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr Val Asp Lys Ile Ala Asp
                165                 170             175

atc tcc atc gtc gtc cca tac atc ggt ctg gct ctg aac atc ggc aac      576
Ile Ser Ile Val Val Pro Tyr Ile Gly Leu Ala Leu Asn Ile Gly Asn
                180             185                 190

gag gca cag aag ggc aac ttc aag gat gcc ctt gag ttg ttg ggt gcc      624
Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala Leu Glu Leu Leu Gly Ala
                195             200                 205

ggt att ttg ttg gag ttc gaa ccc gag ctg ctg atc cct acc atc ctg      672
Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu Leu Ile Pro Thr Ile Leu
        210             215                 220

gtc ttc acg atc aag tcc ttc ctg ggt tcc tcc gac aac aag aac aag      720
Val Phe Thr Ile Lys Ser Phe Leu Gly Ser Ser Asp Asn Lys Asn Lys
225             230                 235                 240

gtc att aag gcc atc aac aac gcc ctg aag gag cgt gac gag aag tgg      768
Val Ile Lys Ala Ile Asn Asn Ala Leu Lys Glu Arg Asp Glu Lys Trp
                245             250                 255

aag gaa gtc tat tcc ttc atc gtc tcg aac tgg atg acc aag atc aac      816
Lys Glu Val Tyr Ser Phe Ile Val Ser Asn Trp Met Thr Lys Ile Asn
                260             265                 270

acc cag ttc aac aag cga aag gag cag atg tac cag gct ctg cag aac      864
Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu Gln Asn
                275             280                 285

cag gtc aac gcc atc aag acc atc atc gag tcc aag tac aac tcc tac      912
Gln Val Asn Ala Ile Lys Thr Ile Ile Glu Ser Lys Tyr Asn Ser Tyr
        290             295                 300

acc ctg gag gag aag aac gag ctt acc aac aag tac gat atc aag cag      960
Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn Lys Tyr Asp Ile Lys Gln
305                 310                 315                 320

atc gag aac gag ctg aac cag aag gtc tcc atc gcc atg aac aac atc      1008
Ile Glu Asn Glu Leu Asn Gln Lys Val Ser Ile Ala Met Asn Asn Ile
                325             330                 335

gac agg ttc ctg acc gag tcc tcc atc tcc tac ctg atg aag ctc atc      1056
Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys Leu Ile
                340             345                 350

aac gag gtc aag atc aac aag ctg cga gag tac gac gag aat gtc aag      1104
Asn Glu Val Lys Ile Asn Lys Leu Arg Glu Tyr Asp Glu Asn Val Lys
                355             360                 365

acg tac ctg ctg aac tac atc atc cag cac gga tcc atc ctg              1146
Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His Gly Ser Ile Leu
        370             375                 380

taa                                                                  1149
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<210> 28
<211> 382
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
      on BoNTE Hn

<400> 28
Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala
 1   5   10   15
Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile
             20   25   30
Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr Glu Asn Asp Leu Asp Gln
             35   40   45
Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu
         50   55   60
Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala Tyr Ile Pro Lys Tyr Asp
65   70   75   80
Ser Asn Gly Thr Ser Asp Ile Glu Gln His Asp Val Asn Glu Leu Asn
             85   90   95
Val Phe Phe Tyr Leu Asp Ala Gln Lys Val Pro Glu Gly Glu Asn Asn
             100   105   110
Val Asn Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu Gln Pro Lys
         115   120   125
Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile Asn Asn Val Asn Lys Pro
         130   135   140
Val Gln Ala Ala Leu Phe Val Ser Trp Ile Gln Gln Val Leu Val Asp
145   150   155   160
Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr Val Asp Lys Ile Ala Asp
             165   170   175
Ile Ser Ile Val Val Pro Tyr Ile Gly Leu Ala Leu Asn Ile Gly Asn
         180   185   190
Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala Leu Glu Leu Leu Gly Ala
         195   200   205
Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu Leu Ile Pro Thr Ile Leu
         210   215   220
Val Phe Thr Ile Lys Ser Phe Leu Gly Ser Ser Asp Asn Lys Asn Lys
225   230   235   240
Val Ile Lys Ala Ile Asn Asn Ala Leu Lys Glu Arg Asp Glu Lys Trp
             245   250   255
Lys Glu Val Tyr Ser Phe Ile Val Ser Asn Trp Met Thr Lys Ile Asn
             260   265   270
Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu Gln Asn
             275   280   285
Gln Val Asn Ala Ile Lys Thr Ile Ile Glu Ser Lys Tyr Asn Ser Tyr
         290   295   300
Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn Lys Tyr Asp Ile Lys Gln
305   310   315   320
Ile Glu Asn Glu Leu Asn Gln Lys Val Ser Ile Ala Met Asn Asn Ile
             325   330   335
Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys Leu Ile
             340   345   350
Asn Glu Val Lys Ile Asn Lys Leu Arg Glu Tyr Asp Glu Asn Val Lys
             355   360   365

Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His Gly Ser Ile Leu
   370   375   380 ·

<210> 29
<211> 1227
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (1)...(1224)

<400> 29
atg gcc cca cca cgt ctg tgt att aga gtc aac aac tca gaa tta ttc   48
Met Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn Ser Glu Leu Phe
 1   5   10   15

ttt gtc gct tcc gag tca agc tac aac gag aac gat att aac aca cct   96
Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro
               20   25   30

aaa gag att gac gat act acc aac cta aac aac aac tac cgg aac aac   144
Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Asn Tyr Arg Asn Asn
           35   40   45

ttg gat gag gtt att ttg gat tac aac tca cag acc atc cct caa att   192
Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Gln Thr Ile Pro Gln Ile
     ·50·   55   60

tcc aac cgt acc tta aac act ctt gtc caa gac aac tcc tac gtt cca   240
Ser Asn Arg Thr Leu Asn Thr Leu Val Gln Asp Asn Ser Tyr Val Pro
 65   70   75   80

aga tac gat tct aac ggt acc tca gag atc gag gag tat gat gtt gtt   288
Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu Tyr Asp Val Val
                   85   90   95

gac ttt aac gtc ttt ttc tat ttg cat gcc cag aag gtg cca gaa ggt   336
Asp Phe Asn Val Phe Phe Tyr Leu His Ala Gln Lys Val Pro Glu Gly
               100   105   110

gaa acc aac atc tca ttg act tct tcc att gat acc gcc ttg ttg gaa   384
Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu
           115   120   125

gag tcc aag gat atc ttc ttt tct tcg gag ttt atc gat act atc aac   432
Glu Ser Lys Asp Ile Phe Phe Ser Ser Glu Phe Ile Asp Thr Ile Asn
       130   135   140

aag cct gtc aac gcc gct ctg ttc att gat tgg att agc aag gtc atc   480
Lys Pro Val Asn Ala Ala Leu Phe Ile Asp Trp Ile Ser Lys Val Ile
145   150   155   160

aga gat ttt acc act gaa gct act caa aag tcc act gtt gat aag att   528

```
Arg Asp Phe Thr Thr Glu Ala Thr Gln Lys Ser Thr Val Asp Lys Ile
            165                 170                 175

gct gac atc tct ttg att gtc ccc tat gtc ggt ctt gct ttg aac atc    576
Ala Asp Ile Ser Leu Ile Val Pro Tyr Val Gly Leu Ala Leu Asn Ile
            180                 185                 190

att att gag gca gaa aag ggt aac ttt gag gag gct ttt gaa ttg ttg    624
Ile Ile Glu Ala Glu Lys Gly Asn Phe Glu Glu Ala Phe Glu Leu Leu
            195                 200                 205

gga gtt ggt att ttg ttg gag ttt gtt cca gaa ctt acc att cct gtc    672
Gly Val Gly Ile Leu Leu Glu Phe Val Pro Glu Leu Thr Ile Pro Val
            210                 215                 220

att tta gtt ttt acg atc aag tcc tac atc gat tca tac gag aac aag    720
Ile Leu Val Phe Thr Ile Lys Ser Tyr Ile Asp Ser Tyr Glu Asn Lys
225                 230                 235                 240

aat aaa gca att aaa gct att aac aac tcc ttg atc gaa aga gag gct    768
Asn Lys Ala Ile Lys Ala Ile Asn Asn Ser Leu Ile Glu Arg Glu Ala
                245                 250                 255

aag tgg aag gaa atc tac tca tgg att gta tca aac tgg ctt act aga    816
Lys Trp Lys Glu Ile Tyr Ser Trp Ile Val Ser Asn Trp Leu Thr Arg
                260                 265                 270

att aac act caa ttt aac aag aga aag gag caa atg tac cag gct ctg    864
Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu
            275                 280                 285

caa aac caa gtc gat gct atc aag act gca att gaa tac aag tac aac    912
Gln Asn Gln Val Asp Ala Ile Lys Thr Ala Ile Glu Tyr Lys Tyr Asn
            290                 295                 300

aac tat act tcc gat gag aag aac aga ctt gaa tct gaa tac aat atc    960
Asn Tyr Thr Ser Asp Glu Lys Asn Arg Leu Glu Ser Glu Tyr Asn Ile
305                 310                 315                 320

aac aac att gaa gaa gag ttg aac aag aaa gtt tct ttg gct atg aag   1008
Asn Asn Ile Glu Glu Glu Leu Asn Lys Lys Val Ser Leu Ala Met Lys
                325                 330                 335

aat atc gaa aga ttt atg acc gaa tcc tct atc tct tac ttg atg aag   1056
Asn Ile Glu Arg Phe Met Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys
            340                 345                 350

ttg atc aat gag gcc aag gtt ggt aag ttg aag aag tac gat aac cac   1104
Leu Ile Asn Glu Ala Lys Val Gly Lys Leu Lys Lys Tyr Asp Asn His
            355                 360                 365

gtt aag agc gat ctg ctg aac tac att ctc gac cac aga tca atc ctg   1152
Val Lys Ser Asp Leu Leu Asn Tyr Ile Leu Asp His Arg Ser Ile Leu
            370                 375                 380

gga gag cag aca aac gag ctg agt gat ttg gtt act tcc act ttg aac   1200
Gly Glu Gln Thr Asn Glu Leu Ser Asp Leu Val Thr Ser Thr Leu Asn
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```
tcc tcc att cca ttt gag ctt tct taa                        1227
Ser Ser Ile Pro Phe Glu Leu Ser
                405
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<210> 30
<211> 408
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
      on BoNTF Hn

<400> 30
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Met Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn Ser Glu Leu Phe
 1               5                  10                  15
Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro
            20                  25                  30
Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Asn Tyr Arg Asn Asn
        35                  40                  45
Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Gln Thr Ile Pro Gln Ile
    50                  55                  60
Ser Asn Arg Thr Leu Asn Thr Leu Val Gln Asp Asn Ser Tyr Val Pro
65                  70                  75                  80
Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu Tyr Asp Val Val
                85                  90                  95
Asp Phe Asn Val Phe Phe Tyr Leu His Ala Gln Lys Val Pro Glu Gly
            100                 105                 110
Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu
        115                 120                 125
Glu Ser Lys Asp Ile Phe Phe Ser Ser Glu Phe Ile Asp Thr Ile Asn
        130                 135                 140
Lys Pro Val Asn Ala Ala Leu Phe Ile Asp Trp Ile Ser Lys Val Ile
145                 150                 155                 160
Arg Asp Phe Thr Thr Glu Ala Thr Gln Lys Ser Thr Val Asp Lys Ile
                165                 170                 175
Ala Asp Ile Ser Leu Ile Val Pro Tyr Val Gly Leu Ala Leu Asn Ile
            180                 185                 190
Ile Ile Glu Ala Glu Lys Gly Asn Phe Glu Glu Ala Phe Glu Leu Leu
        195                 200                 205
Gly Val Gly Ile Leu Leu Glu Phe Val Pro Glu Leu Thr Ile Pro Val
    210                 215                 220
Ile Leu Val Phe Thr Ile Lys Ser Tyr Ile Asp Ser Tyr Glu Asn Lys
225                 230                 235                 240
Asn Lys Ala Ile Lys Ala Ile Asn Asn Ser Leu Ile Glu Arg Glu Ala
            245                 250                 255
Lys Trp Lys Glu Ile Tyr Ser Trp Ile Val Ser Asn Trp Leu Thr Arg
            260                 265                 270
Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu
            275                 280                 285
Gln Asn Gln Val Asp Ala Ile Lys Thr Ala Ile Glu Tyr Lys Tyr Asn
        290                 295                 300
Asn Tyr Thr Ser Asp Glu Lys Asn Arg Leu Glu Ser Glu Tyr Asn Ile
305                 310                 315                 320
```

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Asn Asn Ile Glu Glu Glu Leu Asn Lys Lys Val Ser Leu Ala Met Lys
            325                 330                 335
Asn Ile Glu Arg Phe Met Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys
            340                 345                 350
Leu Ile Asn Glu Ala Lys Val Gly Lys Leu Lys Lys Tyr Asp Asn His
            355                 360                 365
Val Lys Ser Asp Leu Leu Asn Tyr Ile Leu Asp His Arg Ser Ile Leu
    370                 375                 380
Gly Glu Gln Thr Asn Glu Leu Ser Asp Leu Val Thr Ser Thr Leu Asn
385                 390                 395                 400
Ser Ser Ile Pro Phe Glu Leu Ser
            405
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<210> 31
<211> 1233
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (1)...(1230)

<400> 31
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atg gcc aaa aat acc ggt aaa tct gaa cag tgt att att gtt aat aat    48
Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn
 1               5                  10                  15

gag gat tta ttt ttc ata gct aat aaa gat agt ttt tca aaa gat tta    96
Glu Asp Leu Phe Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu
             20                  25                  30

gct aaa gca gaa act ata gca tat aat aca caa aat aat act ata gaa   144
Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu
             35                  40                  45

aat aat ttt tct ata gat cag ttg att tta gat aat gat tta agc agt   192
Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser
     50                  55                  60

ggc ata gac tta cca aat gaa aac aca gaa cca ttt aca aat ttt gac   240
Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp
 65                  70                  75                  80

gac ata gat atc cct gtg tat att aaa caa tct gct tta aaa aaa att   288
Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Lys Ile
                 85                  90                  95

ttt gtg gat gga gat agc ctt ttt gaa tat tta cat gct caa aca ttt   336
Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe
             100                 105                 110

cct tct aat ata gaa aat cta caa cta acg aat tca tta aat gat gct   384
Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala
             115                 120                 125
```

```
tta aga aat aat aat aaa gtc tat act ttt ttt tct aca aac ctt gtt    432
Leu Arg Asn Asn Asn Lys Val Tyr Thr Phe Phe Ser Thr Asn Leu Val
    130             135             140

gaa aaa gct aat aca gtt gta ggt gct tca ctt ttt gta aac tgg gta    480
Glu Lys Ala Asn Thr Val Val Gly Ala Ser Leu Phe Val Asn Trp Val
145             150             155             160

aaa gga gta ata gat gat ttt aca tct gaa tcc aca caa aaa agt act    528
Lys Gly Val Ile Asp Asp Phe Thr Ser Glu Ser Thr Gln Lys Ser Thr
                165             170             175

ata gat aaa gtt tca gat gta tcc ata att att ccc tat ata gga cct    576
Ile Asp Lys Val Ser Asp Val Ser Ile Ile Ile Pro Tyr Ile Gly Pro
            180             185             190

gct ttg aat gta gga aat gaa aca gct aaa gaa aat ttt aaa aat gct    624
Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Glu Asn Phe Lys Asn Ala
        195             200             205

ttt gaa ata ggt gga gcc gct atc tta atg gag ttt att cca gaa ctt    672
Phe Glu Ile Gly Gly Ala Ala Ile Leu Met Glu Phe Ile Pro Glu Leu
    210             215             220

att gta cct ata gtt gga ttt ttt aca tta gaa tca tat gta gga aat    720
Ile Val Pro Ile Val Gly Phe Phe Thr Leu Glu Ser Tyr Val Gly Asn
225             230             235             240

aaa ggg cat att att atg acg ata tcc aat gct tta aag aaa agg gat    768
Lys Gly His Ile Ile Met Thr Ile Ser Asn Ala Leu Lys Lys Arg Asp
                245             250             255

caa aaa tgg aca gat atg tat ggt ttg ata gta tcg cag tgg ctc tca    816
Gln Lys Trp Thr Asp Met Tyr Gly Leu Ile Val Ser Gln Trp Leu Ser
                260             265             270

acg gtt aat act caa ttt tat aca ata aaa gaa aga atg tac aat gct    864
Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Arg Met Tyr Asn Ala
            275             280             285

tta aat aat caa tca caa gca ata gaa aaa ata ata gaa gat caa tat    912
Leu Asn Asn Gln Ser Gln Ala Ile Glu Lys Ile Ile Glu Asp Gln Tyr
    290             295             300

aat aga tat agt gaa gaa gat aaa atg aat att aac att gat ttt aat    960
Asn Arg Tyr Ser Glu Glu Asp Lys Met Asn Ile Asn Ile Asp Phe Asn
305             310             315             320

gat ata gat ttt aaa ctt aat caa agt ata aat tta gca ata aac aat   1008
Asp Ile Asp Phe Lys Leu Asn Gln Ser Ile Asn Leu Ala Ile Asn Asn
            325             330             335

ata gat gat ttt ata aac caa tgt tct ata tca tat cta atg aat aga   1056
Ile Asp Asp Phe Ile Asn Gln Cys Ser Ile Ser Tyr Leu Met Asn Arg
            340             345             350
```

```
atg att cca tta gct gta aaa aag tta aaa gac ttt gat gat aat ctt      1104
Met Ile Pro Leu Ala Val Lys Lys Leu Lys Asp Phe Asp Asp Asn Leu
        355                 360                 365

aag aga gat tta ttg gag tat ata gat aca aat gaa cta tat tta ctt      1152
Lys Arg Asp Leu Leu Glu Tyr Ile Asp Thr Asn Glu Leu Tyr Leu Leu
    370                 375                 380

gat gaa gta aat att cta aaa tca aaa gta aat aga cac cta aaa gac      1200
Asp Glu Val Asn Ile Leu Lys Ser Lys Val Asn Arg His Leu Lys Asp
385                 390                 395                 400

agt ata cca ttt gat ctt tca cta tat acc taa                          1233
Ser Ile Pro Phe Asp Leu Ser Leu Tyr Thr
                405                 410


<210> 32
<211> 410
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
      on BoNTG Hn

<400> 32
Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn
1               5                   10                  15
Glu Asp Leu Phe Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu
            20                  25                  30
Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu
        35                  40                  45
Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser
    50                  55                  60
Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp
65                  70                  75                  80
Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Lys Ile
                85                  90                  95
Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe
            100                 105                 110
Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala
        115                 120                 125
Leu Arg Asn Asn Asn Lys Val Tyr Thr Phe Phe Ser Thr Asn Leu Val
    130                 135                 140
Glu Lys Ala Asn Thr Val Val Gly Ala Ser Leu Phe Val Asn Trp Val
145                 150                 155                 160
Lys Gly Val Ile Asp Asp Phe Thr Ser Glu Ser Thr Gln Lys Ser Thr
                165                 170                 175
Ile Asp Lys Val Ser Asp Val Ser Ile Ile Ile Pro Tyr Ile Gly Pro
            180                 185                 190
Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Glu Asn Phe Lys Asn Ala
        195                 200                 205
Phe Glu Ile Gly Gly Ala Ala Ile Leu Met Glu Phe Ile Pro Glu Leu
    210                 215                 220
Ile Val Pro Ile Val Gly Phe Phe Thr Leu Glu Ser Tyr Val Gly Asn
225                 230                 235                 240
```

```
Lys Gly His Ile Ile Met Thr Ile Ser Asn Ala Leu Lys Lys Arg Asp
            245                 250                 255
Gln Lys Trp Thr Asp Met Tyr Gly Leu Ile Val Ser Gln Trp Leu Ser
            260                 265                 270
Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Arg Met Tyr Asn Ala
            275                 280         .       285
Leu Asn Asn Gln Ser Gln Ala Ile Glu Lys Ile Ile Glu Asp Gln Tyr
        290                 295                 300
Asn Arg Tyr Ser Glu Glu Asp Lys Met Asn Ile Asn Ile Asp Phe Asn
305                 310                 315                 320
Asp Ile Asp Phe Lys Leu Asn Gln Ser Ile Asn Leu Ala Ile Asn Asn
            325                 330                 335
Ile Asp Asp Phe Ile Asn Gln Cys Ser Ile Ser Tyr Leu Met Asn Arg
            340                 345                 350
Met Ile Pro Leu Ala Val Lys Lys Leu Lys Asp Phe Asp Asp Asn Leu
            355                 360                 365
Lys Arg Asp Leu Leu Glu Tyr Ile Asp Thr Asn Glu Leu Tyr Leu Leu
            370                 375                 380
Asp Glu Val Asn Ile Leu Lys Ser Lys Val Asn Arg His Leu Lys Asp
385                 390                 395                 400
Ser Ile Pro Phe Asp Leu Ser Leu Tyr Thr
            405                 410
```

𝒶 <210> 33
<211> 1314
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (10)...(1305)

<400> 33

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gaattcacg atg tct tac act aac gac aaa atc ctg atc ctg tac ttc aac   51
          Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn
           1               5                   10

aaa ctg tac aaa aaa atc aaa gac aac tct atc ctg gac atg cgt tac   99
Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr
 15             20              25                  30

gaa aac aac aaa ttc atc gac atc tct ggc tat ggt tct aac atc tct  147
Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser
                35              40                  45

atc aac ggt gac gtc tac atc tac tct act aac cgc aac cag ttc ggt  195
Ile Asn Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly
            50                  55                  60

atc tac tct tct aaa ccg tct gaa gta aac atc gct cag aac aac gac  243
Ile Tyr Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp
        65                  70                  75

atc atc tac aac ggt cgt tac cag aac ttc tct atc tct ttc tgg gtt  291
```

```
Ile Ile Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val
     80                      85                   90

cgt atc ccg aaa tac ttc aac aaa gtt aac ctg aac aac gaa tac act    339
Arg Ile Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr
 95              100                 105                 110

atc atc gac tgc atc cgt aac aac aac tct ggt tgg aaa atc tct ctg    387
Ile Ile Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu
             115                 120                 125

aac tac aac aaa atc atc tgg act ctg cag gac act gct ggt aac aac    435
Asn Tyr Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn
             130                 135                 140

cag aaa ctg gtt ttc aac tac act cag atg atc tct atc tct gac tac    483
Gln Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr
             145                 150                 155

att aat aaa tgg atc ttc gtt act atc act aac aac cgt ctg ggt aac    531
Ile Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn
         160                 165                 170

tct cgt atc tac atc aac ggt aac ctg atc gat gaa aaa tct atc tct    579
Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser
175             180                 185                 190

aac ctg ggt gac atc cac gtt tct gac aac atc ctg ttc aaa atc gtt    627
Asn Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val
                 195                 200                 205

ggt tgc aac gac acg cgt tac gtt ggt atc cgt tac ttc aaa gtt ttc    675
Gly Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe
             210                 215                 220

gac act gaa ctg ggt aaa act gaa atc gaa act ctg tac tct gac gaa    723
Asp Thr Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu
             225                 230                 235

ccg gac ccg tct atc ctg aaa gac ttc tgg ggt aac tac ctg ctg tac    771
Pro Asp Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr
     240                 245                 250

aac aaa cgt tac tac ctg ctc aac ctg ctc cgg act gac aaa tct atc    819
Asn Lys Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile
255                 260                 265                 270

act cag aac tct aac ttc ctg aac atc aac cag cag cgt ggt gtt tat    867
Thr Gln Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr
             275                 280                 285

cag aaa cct aat atc ttc tct aac act cgt ctg tac act ggt gtt gaa    915
Gln Lys Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu
             290                 295                 300

gtt atc atc cgt aaa aac ggt tct act gac atc tct aac act gac aac    963
Val Ile Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn
```

```
ttc gta cgt aaa aac gac ctg gct tac atc aac gtt gtt gac cgt gac    1011
Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp
    320                     325                     330

gtt gaa tac cgt ctg tac gct gac atc tct atc gct aaa ccg gaa aaa    1059
Val Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys
335                     340                     345                 350

atc atc aaa ctg atc cgt act tct aac tct aac aac tct ctg ggt cag    1107
Ile Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln
                355                     360                     365

atc atc gtt atg gac tcg atc ggt aac aac tgc act atg aac ttc cag    1155
Ile Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln
                370                     375                     380

aac aac aac ggt ggt aac atc ggt ctg ctg ggt ttc cac tct aac aac    1203
Asn Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn
            385                     390                     395

ctg gtt gct tct tca tgg tac tac aac aac atc cgt aaa aac act tct    1251
Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser
        400                     405                     410

tct aac ggt tgc ttc tgg tct ttc atc tct aaa gaa cac ggt tgg cag    1299
Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln
415                     420                     425                 430

gaa aac taagaattc                                                   1314
Glu Asn
```

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<210> 34
<211> 432
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
      on BoNTF Hc

<400> 34
Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu
1               5                   10                  15
Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn
            20                  25                  30
Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn
        35                  40                  45
Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr
    50                  55                  60
Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile
65                  70                  75                  80
Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile
                85                  90                  95
```

```
Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile
            100                 105                 110
Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr
            115                 120                 125
Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys
        130                 135                 140
Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn
145                 150                 155                 160
Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg
                165                 170                 175
Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu
            180                 185                 190
Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys
        195                 200                 205
Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr
        210                 215                 220
Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp
225                 230                 235                 240
Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys
                245                 250                 255
Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln
                260                 265                 270
Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys
        275                 280                 285
Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile
        290                 295                 300
Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val
305                 310                 315                 320
Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu
                325                 330                 335
Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile
                340                 345                 350
Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile
        355                 360                 365
Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn
        370                 375                 380
Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val
385                 390                 395                 400
Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn
                405                 410                 415
Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn
                420                 425                 430


<210> 35
<211> 1278
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (10)...(1269)

<400> 35
ttcgaaacg atg att tta att tcc tac ttc aac aag ttc ttc aag aga att 51
```

```
                 Met Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile
                  1                 5                   10

aag tct tct tcc gtt tta aac atg aga tac aag aat gat aaa tac gtc   99
Lys Ser Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val
 15                  20                  25                  30

gac act tcc ggt tac gac tcc aat atc aac att aac ggt gac gtg tac  147
Asp Thr Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr
                     35                  40                  45

aag tac cca act aac aaa aac caa ttc ggt atc tac aac gac aag ctt  195
Lys Tyr Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu
                 50                  55                  60

act gag ctg aac atc tct caa aac gac tac att atc tac gac aac aag  243
Thr Glu Leu Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys
             65                  70                  75

tac aat aac ttc tct att tct ttc tgg gtc aga att cct aac tac gat  291
Tyr Asn Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp
     80                  85                  90

aac aag atc gtc aac gtt aac aac gag tac act atc atc aac tgt atg  339
Asn Lys Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met
 95                  100                 105                 110

aga gac aac aac tcc ggt tgg aag gtc tct ctt aac cac aac gag atg  387
Arg Asp Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Met
                 115                 120                 125

att tgg acc ttg caa gac aac gca ggt att aac caa aag tta gca ttc  435
Ile Trp Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe
             130                 135                 140

aac tac ggt aac gca aac ggt att tct gac tac atc aac aag tgg att  483
Asn Tyr Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile
             145                 150                 155

ttc gtc act atc act aac gac aga tta ggg gac tct aag ctt tac att  531
Phe Val Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile
     160                 165                 170

aac ggt aac tta atc gac caa aag tcc att tta aac tta ggt aac att  579
Asn Gly Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile
175                 180                 185                 190

cac gtt tct gac aac atc tta ttc aag atc gtt aac tgc agt tac aac  627
His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Asn
                 195                 200                 205

aga tac att ggc att aga tac ttc aac att ttc gac aag gag tta gac  675
Arg Tyr Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp
                 210                 215                 220

gag acc gag att caa act tta tac agc aac gaa cct aac acc aat att  723
Glu Thr Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile
```

```
                  225                      230                        235

ttg aag gac ttc tgg ggt aac tac ttg ctt tac gac aag gaa tac tac      771
Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr
        240                      245                  250

tta tta aac gtg tta aag cca aac aac ttc att gat agg aga aag gat      819
Leu Leu Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp
255                      260                  265                  270

tct act tta agc att aac aac atc aga agc act att ctt tta gct aac      867
Ser Thr Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn
                    275              280                  285

aga tta tac tct ggt atc aag gtt aag atc caa aga gtt aac aac tct      915
Arg Leu Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser
                290                  295                  300

tct act aac gat aac ctt gtt aga aag aac gat cag gtc tat att aac      963
Ser Thr Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn
            305                  310                  315

ttc gtc gct agc aag act cac tta ttc cca tta tat gct gat aac gct     1011
Phe Val Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Asn Ala
        320                  325                  330

acc acc aac aag gag aag acc atc aag atc tcc tcc tct ggc aac aga     1059
Thr Thr Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg
335                  340                  345                  350

ttt aac caa gtc gtc gtt atg aac tcc gtc ggt aac aac tgt acc atg     1107
Phe Asn Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met
                355                  360                  365

aac ttt aaa aat aat aat gga aat aat att ggg tgt tta ggt ttc aag     1155
Asn Phe Lys Asn Asn Asn Gly Asn Asn Ile Gly Cys Leu Gly Phe Lys
            370                  375                  380

gca gat act gta gtt gct agt act tgg tat tat acc cac atg aga gat     1203
Ala Asp Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp
            385                  390                  395

cac acc aac agc aat gga tgt ttt tgg aac ttt att tct gaa gaa cat     1251
His Thr Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His
            400                  405                  410

gga tgg caa gaa aaa taa tagggatcc                                   1278
Gly Trp Gln Glu Lys  *
415


<210> 36
<211> 419
<212> PRT
<213> Artificial Sequence

<220>
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<223> Encoded polypeptide of a synthetic construct based
       on BoNTE Hc

<400> 36
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Met Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser
1               5                  10                 15
Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr
            20                  25                 30
Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr
        35                  40                 45
Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Thr Glu
        50                  55                 60
Leu Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys
65                  70                 75                 80
Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys
                85                  90                 95
Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp
                100                 105                110
Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp
            115                 120                 125
Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr
    130                 135                 140
Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val
145                 150                 155                 160
Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly
                165                 170                 175
Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val
            180                 185                 190
Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr
        195                 200                 205
Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr
    210                 215                 220
Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys
225                 230                 235                 240
Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu
            245                 250                 255
Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr
            260                 265                 270
Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu
        275                 280                 285
Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr
    290                 295                 300
Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val
305                 310                 315                 320
Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr
            325                 330                 335
Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn
        340                 345                 350
Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe
        355                 360                 365
Lys Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp
    370                 375                 380
Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr
385                 390                 395                 400
Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp
                405                 410                 415
Gln Glu Lys
```

<210> 37
<211> 1338
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<221> CDS
<222> (9)...(1325)

<400> 37
```
ctcgagcc atg gct cgt ctg ctg tct acc ttc act gaa tac atc aag aac      50
        Met Ala Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn
          1               5                   10

atc atc aat acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg       98
Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu
 15                  20                  25                  30

atc gac ctg tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt      146
Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val
                35                  40                  45

aac ttc gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa      194
Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu
            50                  55                  60

tct tcc aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct      242
Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser
            65                  70                  75

atg tac gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac      290
Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr
        80                  85                  90

ttc aac tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg      338
Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met
 95                 100                 105                 110

gaa aac aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc      386
Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile
                115                 120                 125

tgg act ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa      434
Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys
                130                 135                 140

tac tct cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc      482
Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe
            145                 150                 155

gtt acc atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac      530
Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn
```

```
ggc cgt ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac    578
Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His
175                 180                 185                 190

gct tct aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac    626
Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His
                    195                 200                 205

cgc tac atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac    674
Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn
                210                 215                 220

gaa aaa gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc    722
Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile
            225                 230                 235

ctg aaa gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac    770
Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr
        240                 245                 250

atg ctg aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta    818
Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val
255                 260                 265                 270

ggt atc cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg    866
Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met
                275                 280                 285

act acc aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc    914
Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe
                290                 295                 300

atc atc aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac    962
Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn
            305                 310                 315

aat gat cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt   1010
Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg
            320                 325                 330

ctg gct acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct   1058
Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala
335                 340                 345                 350

ctg gaa atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa   1106
Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys
                355                 360                 365

tcc aag aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag   1154
Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln
            370                 375                 380

gac aac aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac   1202
Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn
            385                 390                 395
```

```
aat atc gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa     1250
Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu
    400                 405                 410

cgt tcc tct cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat     1298
Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp
415                 420                 425                 430

gac ggt tgg ggt gaa cgt ccg ctg taa cccgggaaag ctt                  1338
Asp Gly Trp Gly Glu Arg Pro Leu  *
                435
```

<210> 38
<211> 415
<212> PRT
<213> Clostridium botulinum

<400> 38

```
Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys
1               5                   10                  15
Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln
        20                  25                  30
Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys
        35                  40                  45
Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe
    50                  55                  60
Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu
65                  70                  75                  80
Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser
                85                  90                  95
Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile
                100                 105                 110
Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp
                115                 120                 125
Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn
    130                 135                 140
Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile
145                 150                 155                 160
Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu
                165                 170                 175
Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Phe Tyr Phe Asn
                180                 185                 190
Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp
                195                 200                 205
Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu
    210                 215     .           220
Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys
225                 230                 235                 240
Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys
                245                 250                 255
Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser
                260                 265                 270
Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn
    275                 280                 285
Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val
```

```
          290                      295                      300
Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly
305                      310                      315                      320
Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu
                    325                      330                      335
Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn
                    340                      345                      350
Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly Phe
               355                      360                      365
Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser Asn
          370                      375                      380
Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys Ser
385                      390                      395                      400
Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu
                    405                      410                      415
```

<210> 39
<211> 1348
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTB Hc

<221> CDS
<222> (1)...(1323)

<400> 39
```
atg gcc aac aaa tac aat tcc gaa atc ctg aac aat atc atc ctg aac    48
Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn
 1               5                  10                  15

ctg cgt tac aaa gac aac aat ctg atc gat ctg tct ggt tac ggt gct    96
Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala
                20                  25                  30

aaa gtt gaa gta tac gac ggt gtt gaa ctg aat gac aag aac cag ttc   144
Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn Gln Phe
            35                  40                  45

aaa ctg acc tct tcc gct aac tct aag atc cgt gtt act cag aat cag   192
Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln Asn Gln
        50                  55                  60

aac atc atc ttc aac tcc gta ttc ctg gac ttc tct gtt tcc ttc tgg   240
Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser Phe Trp
 65                  70                  75                  80

atc cgt atc ccg aaa tac aag aac gac ggt atc cag aat tac atc cac   288
Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr Ile His
                85                  90                  95

aat gaa tac acc atc atc aac tgc atg aag aat aac tct ggt tgg aag   336
Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly Trp Lys
            100                 105                 110
```

```
atc tcc atc cgc ggt aac cgt atc atc tgg act ctg atc gat atc aac    384
Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Ile Asn
        115                 120                 125

ggt aag acc aaa tct gta ttc ttc gaa tac aac atc cgt gaa gac atc    432
Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile
        130                 135                 140

tct gaa tac atc aat cgc tgg ttc ttc gtt acc atc acc aat aac ctg    480
Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn Asn Leu
145                 150                 155                 160

aac aat gct aaa atc tac atc aac ggt aaa ctg gaa tct aat acc gac    528
Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp
                165                 170                 175

atc aaa gac atc cgt gaa gtt atc gct aac ggt gaa atc atc ttc aaa    576
Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys
                180                 185                 190

ctg gac ggt gac atc gat cgt acc cag ttc atc tgg atg aaa tac ttc    624
Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe
        195                 200                 205

tcc atc ttc aac acc gaa ctg tct cag tcc aat atc gaa gaa cgg tac    672
Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr
    210                 215                 220

aag atc cag tct tac tcc gaa tac ctg aaa gac ttc tgg ggt aat ccg    720
Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro
225                 230                 235                 240

ctg atg tac aac aaa gaa tac tat atg ttc aat gct ggt aac aag aac    768
Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn
                245                 250                 255

tct tac atc aaa ctg aag aaa gac tct ccg gtt ggt gaa atc ctg act    816
Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Thr
                260                 265                 270

cgt tcc aaa tac aac cag aac tct aaa tac atc aac tac cgc gac ctg    864
Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu
        275                 280                 285

tac atc ggt gaa aag ttc atc atc cgt cgc aaa tct aac tct cag tcc    912
Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser
        290                 295                 300

atc aat gat gac atc gta cgt aaa gaa gac tac atc tac ctg gac ttc    960
Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe
305                 310                 315                 320

ttc aac ctg aat cag gaa tgg cgt gta tac acc tac aag tac ttc aag   1008
Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr Phe Lys
                325                 330                 335

aaa gaa gaa gaa aag ctt ttc ctg gct ccg atc tct gat tcc gac gaa   1056
```

```
Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu
        340              345              350

ctc tac aac acc atc cag atc aaa gaa tac gac gaa cag ccg acc tac    1104
Leu Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro Thr Tyr
        355              360              365

tct tgc cag ctg ctg ttc aag aaa gat gaa gaa tct act gac gaa atc    1152
Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile
    370              375              380

ggt ctg atc ggt atc cac cgt ttc tac gaa tct ggt atc gta ttc gaa    1200
Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu
385              390              395              400

gaa tac aaa gac tac ttc tgc atc tcc aaa tgg tac ctg aag gaa gtt    1248
Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val
            405              410              415

aaa cgc aaa ccg tac aac ctg aaa ctg ggt tgc aat tgg cag ttc atc    1296
Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile
            420              425              430

ccg aaa gac gaa ggt tgg acc gaa tag taacctctag agtcgaggcc          1343
Pro Lys Asp Glu Gly Trp Thr Glu  *
        435              440

tgcag                                                              1348

<210> 40
<211> 436
<212> PRT
<213> Clostridium botulinum

<400> 40
Phe Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn Leu
 1           5               10              15
Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala Lys
        20              25              30
Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn Gln Phe Lys
        35              40              45
Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln Asn Gln Asn
    50              55              60
Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser Phe Trp Ile
65              70              75              80
Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr Ile His Asn
            85              90              95
Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly Trp Lys Ile
            100             105             110
Ser Ile Arg Gly Asn Arg Ile Trp Thr Leu Ile Asp Ile Asn Gly Lys
        115             120             125
Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile Ser Glu
    130             135             140
Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn Asn Leu Asn Asn
145             150             155             160
Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp Ile Lys
            165             170             175
```

```
Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys Leu Asp
        180                 185                 190
Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe Ser Ile
        195                 200                 205
Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr Lys Ile
        210                 215                 220
Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro Leu Met
225                 230                 235                 240
Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn Ser Tyr
                245                 250                 255
Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Thr Arg Ser
        260                 265                 270
Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu Tyr Ile
        275                 280                 285
Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser Ile Asn
        290                 295                 300
Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe Phe Asn
305                 310                 315                 320
Leu Asn Gln Glu Arg Val Tyr Thr Tyr Lys Phe Lys Lys Glu Glu Glu
                325                 330                 335
Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu Phe Tyr Asn Thr
                340                 345                 350
Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro Thr Tyr Ser Cys Gln Leu
        355                 360                 365
Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile Gly Leu Ile Gly
        370                 375                 380
Ile His Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu Glu Tyr Lys Asp
385                 390                 395                 400
Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val Lys Arg Lys Pro
                405                 410                 415
Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile Pro Lys Asp Glu
                420                 425                 430
Gly Trp Thr Glu
        435


<210> 41
<211> 848
<212> PRT
<213> Clostridium botulinum

<400> 41
Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
 1               5                   10                  15
Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu
            20                  25                  30
Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
            35                  40                  45
Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro
        50                  55                  60
Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
65                  70                  75                  80
Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
                85                  90                  95
Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu
            100                 105                 110
His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu
```

```
              115                    120                    125
Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys
    130                    135                    140
Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu
145                    150                    155                    160
Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr
                   165                    170                    175
Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala
                   180                    185                    190
Leu Asn Ile Gly Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu Ile
                   195                    200                    205
Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala Ile
    210                    215                    220
Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys Val
225                    230                    235                    240
Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu Lys
                   245                    250                    255
Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys Val
                   260                    265                    270
Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu Glu
    275                    280                    285
Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn Gln
    290                    295                    300
Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp Leu
305                    310                    315                    320
Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile Asn
                   325                    330                    335
Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile
                   340                    345                    350
Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys Asp
                   355                    360                    365
Ala Leu Leu Lys Tyr Ile Arg Asp Asn Tyr Gly Thr Leu Ile Gly Gln
    370                    375                    380
Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp Ile
385                    390                    395                    400
Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser Thr
                   405                    410                    415
Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu
                   420                    425                    430
Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys
                   435                    440                    445
Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln
    450                    455                    460
Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys
465                    470                    475                    480
Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe
                   485                    490                    495
Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu
                   500                    505                    510
Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser
                   515                    520                    525
Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile
    530                    535                    540
Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp
545                    550                    555                    560
Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn
                   565                    570                    575
```

```
Asn Ser Lys Ile Tyr Thr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro
        580                 585                 590
Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys
        595                 600                 605
Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe
        610                 615                 620
Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr
625                 630                 635                 640
Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr
                645                 650                 655
Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Ile Leu Leu Tyr Asp Pro Asn
                660                 665                 670
Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu
                675                 680                 685
Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser
        690                 695                 700
Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly
705                 710                 715                 720
Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val
                725                 730                 735
Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala
                740                 745                 750
Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn
        755                 760                 765
Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr
        770                 775                 780
Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
785                 790                 795                 800
Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser
                805                 810                 815
Asn Trp Tyr Asn Arg Gln Thr Glu Arg Ser Ser Arg Thr Leu Gly Cys
                820                 825                 830
Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu
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<400> 42
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        20                  25                  30
Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile Asn
        35                  40                  45
Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro Ser
        50                  55                  60
Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val Tyr
65                  70                  75                  80
Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr Ile
                85                  90                  95
Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp Ile
        100                 105                 110
Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys Val
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                    115                     120                     125
Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val Val
    130                     135                     140
Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp Phe
145                     150                     155                     160
Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp Ile
                    165                     170                     175
Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn Glu
                    180                     185                     190
Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala Ser
            195                     200                     205
Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly Ala
    210                     215                     220
Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys Thr
225                     230                     235                     240
Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met Tyr
                    245                     250                     255
Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe Tyr
                    260                     265                     270
Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln Ala
            275                     280                     285
Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys Glu
    290                     295                     300
Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu Asn
305                     310                     315                     320
Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn Gly
                    325                     330                     335
Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val Glu
                    340                     345                     350
Lys Leu Leu Asp Phe Asp Asn Thr Leu Lys Lys Asn Leu Leu Asn Tyr
            355                     360                     365
Ile Asp Glu Asn Lys Leu Tyr Leu Ile Gly Ser Ala Glu Tyr Glu Lys
    370                     375                     380
Ser Lys Val Asn Lys Tyr Leu Lys Thr Ile Met Pro Phe Asp Leu Ser
385                     390                     395                     400
Ile Tyr Thr Asn Asp Thr Ile Leu Ile Glu Met Phe Asn Lys Tyr Asn
                    405                     410                     415
Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn Leu Arg Tyr Lys Asp Asn
            420                     425                     430
Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala Lys Val Glu Val Tyr Asp
            435                     440                     445
Gly Val Glu Leu Asn Asp Lys Asn Gln Phe Lys Leu Thr Ser Ser Ala
    450                     455                     460
Asn Ser Lys Ile Arg Thr Gln Asn Gln Asn Ile Ile Phe Asn Ser Val
465                     470                     475                     480
Phe Leu Asp Phe Ser Val Ser Phe Trp Ile Arg Ile Pro Lys Tyr Lys
            485                     490                     495
Asn Asp Gly Ile Gln Asn Tyr Ile His Asn Glu Tyr Thr Ile Ile Asn
            500                     505                     510
Cys Met Lys Asn Asn Ser Gly Trp Lys Ile Ser Ile Arg Gly Arg Ile
    515                     520                     525
Ile Trp Thr Leu Ile Asp Ile Asn Gly Lys Thr Lys Ser Val Phe Phe
    530                     535                     540
Glu Tyr Asn Ile Arg Glu Asp Ile Ser Glu Tyr Ile Asn Arg Trp Phe
545                     550                     555                     560
Phe Val Thr Ile Thr Asn Asn Leu Asn Asn Ala Lys Ile Tyr Ile Asn
                    565                     570                     575
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Gly Lys Leu Glu Ser Asn Thr Asp Ile Lys Asp Ile Arg Glu Val Ile
        580                 585                 590
Ala Asn Gly Glu Ile Ile Phe Lys Leu Asp Gly Asp Ile Asp Arg Thr
        595                 600                 605
Gln Phe Ile Trp Met Lys Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser
    610                 615                 620
Gln Ser Asn Ile Glu Glu Arg Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr
625                 630                 635                 640
Leu Lys Asp Phe Trp Gly Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr
            645                 650                 655
Met Phe Asn Ala Gly Asn Lys Asn Ser Tyr Ile Lys Leu Lys Lys Asp
            660                 665                 670
Ser Pro Val Gly Glu Ile Leu Thr Arg Ser Lys Tyr Asn Gln Asn Ser
        675                 680                 685
Lys Tyr Ile Asn Tyr Arg Asp Leu Tyr Ile Gly Glu Lys Phe Ile Ile
        690                 695                 700
Arg Arg Lys Ser Asn Ser Gln Ser Ile Asn Asp Asp Ile Val Arg Lys
705                 710                 715                 720
Glu Asp Tyr Ile Tyr Leu Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg
            725                 730                 735
Val Tyr Thr Tyr Lys Tyr Phe Lys Lys Glu Glu Glu Leu Phe Leu Ala
            740                 745                 750
Pro Ile Ser Asp Ser Asp Glu Phe Tyr Asn Thr Ile Gln Ile Lys Glu
        755                 760                 765
Tyr Asp Glu Gln Pro Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp
        770                 775                 780
Glu Glu Ser Thr Asp Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr
785                 790                 795                 800
Glu Ser Gly Ile Val Phe Glu Glu Lys Asp Phe Cys Ile Ser Trp Tyr
            805                 810                 815
Leu Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp
            820                 825                 830
Gln Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu
        835                 840
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